STIC Search Report
Biotech-Chem Library

STIC Database Tracking Number: 184731

TO: Minh-Tam Davis **Location: REM/3a24/3c18** **Art Unit: 1642** April 12, **2006** **Case Serial Number:** 09/277064	**From: P. Sheppard** **Location: Remsen Building** **Phone: (571) 272-2529** **sheppard@uspto.gov**

Search Notes

73622 184731 MG

STIC-Biotech/ChemLib

From: Chan, Christina
Sent: Monday, April 10, 2006 8:16 AM
To: Davis, Minh-Tam; STIC-Biotech/ChemLib
Subject: RE: Rush search request for 09/277064

RECEIVED
APR 10 2006
TECH CENTER 1600/2900
(STIC)

Please rush. Thanks Chris

Chris Chan
TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

-----Original Message-----
From: Davis, Minh-Tam
Sent: Friday, April 07, 2006 12:27 PM
To: Chan, Christina
Subject: Rush search request for 09/277064

Please search in commercial database, issued patent files and PGPUB:
SEQ ID NO:12, with size limitation to the size of the sequence.
Thank you.
MINH TAM DAVIS
ART UNIT 1642, ROOM 3A24, MB 3C18
27-0830

****
Searcher:_____
Searcher Phone:_____
Date Searcher Picked up:_____
Date completed:_____
Searcher Prep Time:_____
Online Time:_____

****
Type of Search
NA#_____ AA#:_____
S/L:_____ Oligomer:_____
Encode/Transl:_____
Structure #:_____Text:____
Inventor:_____ Litigation:___

****
Vendors and cost where applicable
STN:_____
DIALOG:_____
QUESTEL/ORBIT:_____
LEXIS/NEXIS:_____
SEQUENCE SYSTEM:_____
WWW/Internet:_____
Other (Specify):_____

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OM protein - protein search, using sw model

Run on: April 11, 2006, 19:27:15 ; Search time 188 Seconds
(without alignments)
23.371 Million cell updates/sec

Title: US-09-277-064-12
Perfect score: 51
Sequence: 1 VMAGVGSPYV 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	51	100.0	10	2	AAR61525	Aar61525 Peptide f
2	51	100.0	10	2	AAR97508	Aar97508 Cytotoxic
3	51	100.0	10	2	AAW36826	Aaw36826 Immunogen
4	51	100.0	10	2	AAW70071	Aaw70071 HER-2/neu
5	51	100.0	10	2	AAW77132	Aaw77132 HER-2/neu
6	51	100.0	10	4	AAB99690	Aab99690 HLA A2 bi
7	51	100.0	10	4	AAG89003	Aag89003 HER2/neu
8	51	100.0	10	4	AAG88772	Aag88772 HER2/neu
9	51	100.0	10	5	ABB76755	Abb76755 Tumour an
10	51	100.0	10	5	AAE26800	Aae26800 Human HLA
11	51	100.0	10	5	AEA36306	Aea36306 Human HER
12	51	100.0	10	6	ABU63012	Abu63012 Human Her
13	51	100.0	10	8	ADE97756	Ade97756 Immunogen
14	51	100.0	10	8	ADM12647	Adm12647 MHC class
15	51	100.0	10	8	ADO38880	Ado38880 Human Her
16	51	100.0	10	8	ADP79761	Adp79761 Human HLA
17	51	100.0	15	3	AAY98861	Aay98861 HLA class
18	51	100.0	15	4	AAG88322	Aag88322 HER2/NEU
19	51	100.0	15	4	AAG88306	Aag88306 HER2/NEU
20	51	100.0	15	4	AAG89058	Aag89058 HER2/neu
21	51	100.0	15	4	AAG89031	Aag89031 Her2/neu
22	51	100.0	15	4	AAG89114	Aag89114 HER2/neu
23	51	100.0	18	5	ABJ04191	Abj04191 Kinase-as
24	51	100.0	18	6	ABU54238	Abu54238 ErbB2 pro
25	51	100.0	18	8	ADK72373	Adk72373 HER-2 pep
26	51	100.0	22	8	ADM12649	Adm12649 Ii-key/hu
27	51	100.0	22	8	ADO38882	Ado38882 Human Her
28	51	100.0	112	8	ADK72377	Adk72377 Human HER
29	51	100.0	265	2	AAY43967	Aay43967 Human pro
30	51	100.0	289	8	ADS87905	Ads87905 HER2/ErbB
31	51	100.0	391	9	AEA39008	Aea39008 Rat Her-2
32	51	100.0	435	8	ADR10480	Adr10480 Human pro
33	51	100.0	470	9	ADY30515	Ady30515 Human spl
34	51	100.0	550	8	ADP80498	Adp80498 Human epi
35	51	100.0	583	5	AAE20483	Aae20483 Human pro
36	51	100.0	587	5	AAE20481	Aae20481 Human pro
37	51	100.0	589	5	AAE20484	Aae20484 Human pro
38	51	100.0	600	5	AAE20482	Aae20482 Human pro
39	51	100.0	671	8	ADK72375	Adk72375 BCG-HER-2
40	51	100.0	815	8	ADT50879	Adt50879 Cancer re
41	51	100.0	835	9	ADY30511	Ady30511 Human spl
42	51	100.0	879	9	ADY30514	Ady30514 Human spl
43	51	100.0	960	9	ADY30513	Ady30513 Human spl
44	51	100.0	970	9	ADY30509	Ady30509 Human spl
45	51	100.0	1042	7	ADM29352	Adm29352 Human nov

ALIGNMENTS

RESULT 1
AAR61525
ID AAR61525 standard; peptide; 10 AA.
XX
AC AAR61525;
XX
DT 25-MAR-2003 (revised)
DT 11-MAY-1995 (first entry)
XX
DE Peptide fragment (1.0738) of c-ERB2 binds HLA-A2.1.
XX
KW antigen; epitope; immunogenic target protein; PSA; HBVc; HBVs; EBV; HIV1;
KW plasma specific antigen; hepatitis B virus; Epstein Barr;
KW human immunodeficiency virus; human papilloma virus; p53; c-ERB2; MAGE-1;
KW melanoma antigen-1; core antigen; surface antigen;
KW pharmaceutical composition; in vivo; ex vivo; therapeutic; diagnostic;
KW MHC class I molecule; major histocompatability complex; HLA-A2.1; 9mer;
KW 10mer; anchor; human leukocyte antigen.
XX
OS Homo sapiens.
XX
PN WO9420127-A1.
XX
PD 15-SEP-1994.
XX
PF 04-MAR-1994; 94WO-US002353.
XX
PR 05-MAR-1993; 93US-00027146.
PR 04-JUN-1993; 93US-00073205.
PR 29-NOV-1993; 93US-00159184.
XX
PA (CYTE-) CYTEL CORP.
XX
PI Grey HM, Sette A, Sidney J, Kast W;
XX
DR WPI; 1994-302678/37.
XX
PT Immunogenic peptide(s) having an HLA-A2.1 binding motif - used for
PT treatment or prophylaxis of cancer, virus infection or autoimmune
PT diseases.
XX
PS Example 5; Page 108; 138pp; English.
XX
CC AAR59496-R61666 are immunogenic 10mer peptides that contain a HLA-A2.1
CC binding motif. These peptides bind HLA-A2.1 and have a binding affinity
CC of at least 1% as compared to a reference peptide (AAR71293). AAR61525
CC has an IC50 of 0.018 and the sequence occurs at position 773 in the human

```
CC   c-ERB2 gene product. Peptides of the invention can induce cytotoxic T
CC   lymphocytes which can react with target cells. They can be used for the
CC   treatment or prophlyaxis of cancer, eg. prostate cancer or lymphoma, etc.
CC   (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 10 AA;

  Query Match           100.0%;  Score 51;  DB 2;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0.013;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db          1 VMAGVGSPYV 10


RESULT 2
AAR97508
ID   AAR97508 standard; peptide; 10 AA.
XX
AC   AAR97508;
XX
DT   11-FEB-1997  (first entry)
XX
DE   Cytotoxic T lymphocyte-activating Her-2/Neu-specific peptide.
XX
KW   p53; Her-2; Neu; aa; amino acid; CTL; cytotoxic T lymphocyte; target;
KW   malignant cell; antigenic; vaccine; immunisation; activation.
XX
OS   Homo sapiens.
XX
PN   WO9618409-A1.
XX
PD   20-JUN-1996.
XX
PF   14-DEC-1995;   95WO-US016415.
XX
PR   14-DEC-1994;   94US-00355558.
XX
PA   (SCRI ) SCRIPPS RES INST.
XX
PI   Sherman LA;
XX
DR   WPI; 1996-300385/30.
XX
PT   In vivo activation of tumour-specific cytotoxic T lymphocytes - by
PT   contacting with polypeptide(s) derived from human p53 or Her-2/Neu
PT   proteins.
XX
PS   Claim 5; Page 124; 158pp; English.
XX
CC   AAR97508 is a peptide capable of activating cytotoxic T lymphocytes
CC   (CTLs) which specifically target malignant cells. The peptide corresponds
CC   to amino acids 773-782 of human Her-2/Neu protein. CTL- activating
CC   peptides can be used in a vaccine for protecting against tumour cell
CC   formation. CTLs activated by the peptides will lyse tumour cells
CC   displaying specific peptides. Antibodies against CTL- activating peptides
CC   are useful for the identification of other similar compounds which may be
CC   useful for treating cancer or virally- infected cells, or for diagnosis.
CC   The peptide and vaccines produced provide immunity to a high percentage
CC   of different ethnic groups, i.e. those with different HLA alleles
XX
SQ   Sequence 10 AA;

  Query Match           100.0%;  Score 51;  DB 2;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0.013;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db          1 VMAGVGSPYV 10


RESULT 3
AAW36826
ID   AAW36826 standard; peptide; 10 AA.
XX
AC   AAW36826;
XX
DT   23-MAR-1998  (first entry)
XX
DE   Immunogenic peptide H7 based on the human Her-2/neu protein.
XX
KW   Her-2/neu protein; human leukocyte antigen A2.1; HLA;
KW   cytotoxic T lymphocyte; CTL; immune response; tumour-associated antigen;
KW   T-cell receptor; TCR; tumour treatment.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9732603-A1.
XX
PD   12-SEP-1997.
XX
PF   05-MAR-1997;   97WO-US003611.
XX
PR   05-MAR-1996;   96US-0012845P.
XX
PA   (SCRI ) SCRIPPS RES INST.
XX
PI   Sherman LA,  Lustgarten J;
XX
DR   WPI; 1997-470496/43.
XX
PT   Nucleic acid encoding variable regions of HLA-restricted non-human T cell
PT   receptor specific for tumour antigen - used to identify tumour antigens
PT   and for tumour therapy.
XX
PS   Example 1; Page 9; 34pp; English.
XX
CC   Synthetic peptides AAW36824-40 are based on the sequence of the human Her
CC   -2/neu protein, wherein each sequence contains the anchor motif for human
CC   leukocyte antigen (HLA) A2.1. The present peptide is based on positions
CC   773-782. The ability of these peptides to inhibit the binding of an
CC   influenza virus matrix protein peptide M1 to HLA A2.1 was measured by
CC   inhibition of lysis by an M1 specific, HLA A2.1 restricted, cytotoxic T
CC   lymphocyte (CTL) clone. The present protein showed 55% inhibition. The
CC   peptides were also tested for their ability to elicit an immune response
CC   in vivo. However, only H3 (AAW36824) and H7 (AAW36826) were able to do
CC   this. H3 and H7 peptides are tumour-associated antigens, and were used to
CC   immunize a transgenic, non-human vertebrate (that has been modified to
CC   express at least one HLA antigen), so that the animal produces CTL which
CC   displays HLA-restricted T-cell receptor (TCR) specificity for the
CC   antigen. Nucleic acid encoding variable regions of the alpha and beta
CC   chains of such TCRs can be amplified from CTLs produced in the above
CC   manner. Cells expressing recombinant TCR are used to identify antigens
CC   associated with a tumour and to treat tumours in humans. Transgenic mice
CC   are a more convenient source of CTL than the tumour-infiltrating
CC   lymphocytes previously used. TCR can be humanised to reduce side-
CC   reactions and short peptide derivatives of TCR are more economical to
CC   produce than TCR itself, particularly when expressed as a single-chain
CC   molecule rather than as a dimer
XX
SQ   Sequence 10 AA;

  Query Match           100.0%;  Score 51;  DB 2;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0.013;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db          1 VMAGVGSPYV 10


RESULT 4
AAW70071
```

ID AAW70071 standard; peptide; 10 AA.
XX
AC AAW70071;
XX
DT 22-OCT-1998 (first entry)
XX
DE HER-2/neu derived HLA-A2.1 binding peptide 19 (residues 773-782).
XX
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
KW human leukocyte antigen; HLA; tumour associated antigen; cancer;
KW antigen presenting cell; APC; immunogenic peptide; immune disorder;
KW viral infection; AIDS; hepatitis; bacterial infection; malaria;
KW fungal infection; tuberculosis; melanoma; HER-2/neu; cerB-2.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9833888-A1.
XX
PD 06-AUG-1998.
XX
PF 30-JAN-1998; 98WO-US001959.
XX
PR 31-JAN-1997; 97US-0036696P.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Tsai V, Southwood S, Sidney J, Sette A, Celis E;
XX
DR WPI; 1998-437445/37.
XX
PT Production of antigen-specific cytotoxic T cells - by incubating
PT immunogenic peptide(s) from antigen that binds class I major
PT histocompatibility complex molecules with pre-treated antigen presenting
PT cells.
XX
PS Example 7; Page 77; 104pp; English.
XX
CC Sequences shown in AAW70053 to AAW70075 represent peptides derived from
CC HER-2/neu (cerB-2) antigen. The peptides can bind to a human leukocyte
CC antigen (HLA), HLA-A2.1 and are used to exemplify the method of invention
CC of producing antigen-specific cytotoxic T cells (CTLs) in vitro. The
CC method comprises contacting immunogenic peptides from an antigen that
CC binds class I major histocompatibility complex (MHC) molecules with
CC antigen presenting cells (APCs) pretreated with pretreatment growth
CC factors, and incubating the APCs with purified CD8 cells in the presence
CC of at least 2 incubation growth factors, thereby producing antigen-
CC specific CTLs. A method for specifically killing target cells in a human
CC patient is also provided which comprises obtaining a fluid sample
CC containing CTLs from a patient, contacting the cytotoxic T cells with
CC APCs pretreated with pre-treatment growth factors, where the APCs
CC comprise class I MHC molecules. The pretreated APCs are incubated with
CC the cytotoxic growth factors, thereby producing activated CTLs which are
CC contacted with a carrier to form a composition. The composition can then
CC be administered to the patient. The activated CTLs can be used for
CC treating cancers, immune disorders, viral infections, AIDS, hepatitis,
CC bacterial infection, fungal infection, malaria or tuberculosis
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 51; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VMAGVGSPYV 10
||||||||||
Db 1 VMAGVGSPYV 10

RESULT 5
AAW77132
ID AAW77132 standard; peptide; 10 AA.
XX
AC AAW77132;
XX
DT 16-NOV-1998 (first entry)
XX
DE HER-2/neu synthetic peptide epitope 2.
XX
KW Tyrosinase; tyrosinase cytotoxic lymphocyte response;
KW cytotoxic T lymphocyte; cysteine-depleted; melanoma.
XX
OS Synthetic.
XX
PN WO9833810-A2.
XX
PD 06-AUG-1998.
XX
PF 29-JAN-1998; 98WO-US001592.
XX
PR 30-JAN-1997; 97US-0037781P.
XX
PA (UYVI-) UNIV VIRGINIA PATENT FOUND.
XX
PI Slingluff CL, Hunt DF, Engelhard VH, Kittlesen D;
XX
DR WPI; 1998-437388/37.
XX
PT Disease specific immunogen - comprises disease specific cytotoxic T
PT lymphocyte epitope used to elicit melanoma specific CTL response.
XX
PS Disclosure; Page 27; 93pp; English.
XX
CC The peptide epitope AAW77119-W77138 were created for human tumour-
CC specific cytotoxic T lymphocyte response. These peptides are are cysteine
CC - depleted mutants of a native disease-specific CTL epitope. The cysteine
CC - depleted CTL epitopes elicit a stronger or more specific CTL response
CC than the native epitope. The epitopes can be used in a disease-specific
CC immunogen to protect a mammal against disease in particular melanomas.
CC The peptides may also be used to screen a sample for the presence of an
CC antigen with the same epitope, or with a different cross-reactive epitope
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 51; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VMAGVGSPYV 10
||||||||||
Db 1 VMAGVGSPYV 10

RESULT 6
AAB99690
ID AAB99690 standard; peptide; 10 AA.
XX
AC AAB99690;
XX
DT 06-SEP-2001 (first entry)
XX
DE HLA A2 binding CTL epitope peptide from Her2/neu SEQ ID NO:11.
XX
KW Human leukocyte antigen A2 binding peptide; HLA class I A2; CTL;
KW cytotoxic T-cell lymphocyte; tumour associated antigen; CEA; HER2/neu;
KW MAGE2; MAGE3; p53; vaccine; cancer; cytostatic; immunomodulator;
KW immunotherapy; immune response.
XX
OS Homo sapiens.
XX
PN WO200141741-A1.
XX
PD 14-JUN-2001.
XX
PF 13-DEC-2000; 2000WO-US034318.
XX

PR 13-DEC-1999; 99US-0170448P.
PR 05-APR-2000; 2000US-00543608.
PR 30-MAY-2000; 2000US-00583200.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Fikes J, Sette A, Sidney J, Southwood S, Celis E, Keogh E;
PI Chesnut R;
XX
DR WPI; 2001-381489/40.
XX
PT Compositions for use in a vaccine for treating, e.g., breast, lung and
PT colon cancer comprises at least one peptide that comprises an isolated
PT epitope of a tumor-associated antigen.
XX
PS Claim 1; Page 76; 86pp; English.
XX
CC The present invention describes a composition (I) comprising at least one
CC peptide that comprises an isolated, prepared epitope consisting of a
CC sequence selected from 25 short amino acid sequences given in AAB99680 to
CC AAB99704. Also described are: (1) a composition (II) comprising one or
CC more peptides, and further comprising at least two epitopes selected from
CC the 25 short amino acid sequences (as above), where each of the one or
CC more peptides comprise less than 50 contiguous amino acids that have 100%
CC identity with a native peptide sequence; and (2) a vaccine composition
CC (III) comprising an epitope selected from the 25 short amino acid
CC sequences (as above) and a pharmaceutical excipient. (I) has cytostatic
CC and immunomodulatory activities and can be used in vaccine production and
CC immunotherapy. The peptide epitope compositions (I)-(II) are useful for
CC monitoring an immune response to a tumour associated antigen or when one
CC or more peptides are combined to create a vaccine (III) that stimulates
CC the cellular arm of the immune system. In particular, the vaccine
CC mediates immune responses against tumours in individuals who bear an
CC allele of the human leukocyte antigen (HLA)-A2 supertype and improve the
CC standard of care for patients being treated for breast, colon, or lung
CC cancer
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 51; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VMAGVGSPYV 10
||||||||||
Db 1 VMAGVGSPYV 10

RESULT 7
AAG89003
ID AAG89003 standard; peptide; 10 AA.
XX
AC AAG89003;
XX
DT 11-SEP-2001 (first entry)
XX
DE HER2/neu epitope HLA-A2 supermotif-bearing peptide #16.
XX
KW Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;
KW immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;
KW tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200141787-A1.
XX
PD 14-JUN-2001.
XX
PF 11-DEC-2000; 2000WO-US033591.
XX
PR 10-DEC-1999; 99US-00458299.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;
PI Keogh E;
XX
DR WPI; 2001-374995/39.
XX
PT An isolated prepared HER2/neu epitope useful in a vaccine for inducing
PT cellular immune responses for the prevention and treatment of cancer.
XX
PS Claim 1; Page 189; 199pp; English.
XX
CC The present invention describes isolated prepared HER2/neu epitopes (I).
CC Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is
CC culture in vitro and binds to a complex of an epitope (I), bound to a
CC human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)
CC and a second epitope and the peptide is less than 50 contiguous amino
CC acids that have 100% identity with a native peptide sequence of HER2/neu;
CC (3) a vaccine composition (III) comprising (II) and a pharmaceutical
CC excipient; (4) an isolated nucleic acid encoding a peptide comprising (I)
CC ; and (5) an isolated nucleic acid encoding (II). (I) has cytostatic and
CC immunostimulant activities, and can be used in vaccines. (I), (II) and
CC (III) are useful for inducing cellular immune responses for the
CC prevention and treatment of cancer. (I) and (II) are useful for
CC monitoring or evaluating an immune response to a tumour-associated
CC antigen when incubated with a T lymphocyte sample form a patient and
CC detecting the presence of bound T lymphocyte to (I) or (II). Epitope
CC based vaccines mean that immunosuppressive epitopes that may be present
CC in whole antigens may be avoided. Selected epitopes may be combined to
CC enhance immunogenicity. The possible pathological side effects caused by
CC infectious agents or whole protein antigen is eliminated. The vaccine
CC provides the ability to direct and focus an immune response to multiple
CC selected antigens from the same pathogen. Epitope-based anti-tumour
CC vaccines provides the opportunity to combine epitopes derived from
CC multiple tumour-associated molecules addressing the problem of tumour-
CC tumour variability and reducing the likelihood of tumour escape due to
CC antigen loss. AAG88266 to AAG89121 represent amino acid sequences used in
CC the exemplification of the present invention
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 51; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VMAGVGSPYV 10
||||||||||
Db 1 VMAGVGSPYV 10

RESULT 8
AAG88772
ID AAG88772 standard; peptide; 10 AA.
XX
AC AAG88772;
XX
DT 11-SEP-2001 (first entry)
XX
DE HER2/neu A2 supermotif crossbinding peptide #16.
XX
KW Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;
KW immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;
KW tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200141787-A1.
XX
PD 14-JUN-2001.
XX
PF 11-DEC-2000; 2000WO-US033591.
XX

PR 10-DEC-1999; 99US-00458299.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;
PI Keogh E;
XX
DR WPI; 2001-374995/39.
XX
PT An isolated prepared HER2/neu epitope useful in a vaccine for inducing
PT cellular immune responses for the prevention and treatment of cancer.
XX
PS Example 2; Page 179; 199pp; English.
XX
CC The present invention describes isolated prepared HER2/neu epitopes (I).
CC Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is
CC culture in vitro and binds to a complex of an epitope (I), bound to a
CC human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)
CC and a second epitope and the peptide is less than 50 contiguous amino
CC acids that have 100% identity with a native peptide sequence of HER2/neu;
CC (3) a vaccine composition (III) comprising (II) and a pharmaceutical
CC excipient; (4) an isolated nucleic acid encoding a peptide comprising (I)
CC ; and (5) an isolated nucleic acid encoding (II). (I) has cytostatic and
CC immunostimulant activities, and can be used in vaccines. (I), (II) and
CC (III) are useful for inducing cellular immune responses for the
CC prevention and treatment of cancer. (I) and (II) are useful for
CC monitoring or evaluating an immune response to a tumour-associated
CC antigen when incubated with a T lymphocyte sample form a patient and
CC detecting the presence of bound T lymphocyte to (I) or (II). Epitope
CC based vaccines mean that immunosuppressive epitopes that may be present
CC in whole antigens may be avoided. Selected epitopes may be combined to
CC enhance immunogenicity. The possible pathological side effects caused by
CC infectious agents or whole protein antigen is eliminated. The vaccine
CC provides the ability to direct and focus an immune response to multiple
CC selected antigens from the same pathogen. Epitope-based anti-tumour
CC vaccines provides the opportunity to combine epitopes derived from
CC multiple tumour-associated molecules addressing the problem of tumour-
CC tumour variability and reducing the likelihood of tumour escape due to
CC antigen loss. AAG88266 to AAG89121 represent amino acid sequences used in
CC the exemplification of the present invention
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 51; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VMAGVGSPYV 10
||||||||||
Db 1 VMAGVGSPYV 10

RESULT 9
ABB76755
ID ABB76755 standard; peptide; 10 AA.
XX
AC ABB76755;
XX
DT 31-MAY-2002 (first entry)
XX
DE Tumour antigen epitope HER-2/neu 773 presented by HLA A2.1.
XX
KW Antiviral; anti-HIV; cytostatic; epitope; HLA A2.1;
KW human leukocyte antigen; immunotherapy; cancer; viral infection; vaccine.
XX
OS Unidentified.
XX
PN FR2812087-A1.
XX
PD 25-JAN-2002.
XX
PF 21-JUL-2000; 2000FR-00009591.
XX
PR 21-JUL-2000; 2000FR-00009591.
XX
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
XX
PI Kosmatopoulos K, Tourdot S, Scardino A, Gross DA;
XX
DR WPI; 2002-189846/25.
XX
PT Identifying subdominant or cryptic epitopes, useful in immunotherapy of
PT cancer and viral infection, comprises testing modified, non-immunogenic
PT peptides for induction of cytotoxic T cells.
XX
PS Example 1; Page 12; 62pp; French.
XX
CC The present invention relates to subdominant/cryptic epitopes that are
CC presented by HLA (human leukocyte antigen) Class I molecule A2.1. The
CC epitopes or chimeric polypeptides containing them and nucleic acid
CC encoding them are useful for preventative or curative immunotherapy of
CC cancer and viral infections, particularly where used as vaccines. The
CC present peptide was used to illustrate the invention
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 51; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VMAGVGSPYV 10
||||||||||
Db 1 VMAGVGSPYV 10

RESULT 10
AAE26800
ID AAE26800 standard; peptide; 10 AA.
XX
AC AAE26800;
XX
DT 13-DEC-2002 (first entry)
XX
DE Human HLA-A2.1 restricted HER-2/neu peptide epitope #6.
XX
KW Human; cancer; breast cancer; ovarian cancer; melanoma; cell therapy;
KW epitope; human leucocyte antigen; HLA-A2.1.
XX
OS Homo sapiens.
XX
PN WO200265992-A2.
XX
PD 29-AUG-2002.
XX
PF 19-FEB-2002; 2002WO-US005748.
XX
PR 20-FEB-2001; 2001US-0270252P.
XX
PA (ORTH) ORTHO-MCNEIL PHARM INC.
XX
PI Degraw J, Moriarty A, Leturcq DJ, Jackson MR, Peterson PA;
PI Heiskala M;
XX
DR WPI; 2002-667033/71.
XX
PT Treating a subject with cancer comprises combining the CD+8 cells, which
PT are stimulated with non-naturally occurring antigen-presenting cell line,
PT with adherent blood monocytes and inoculating the subject with CD8+
PT suspension.
XX
PS Example 2; Page 92; 99pp; English.
XX
CC The invention relates to a method of treating a subject with cancer. The
CC method involves combining the CD+8 cells, which are stimulated with non
CC naturally occurring antigen-presenting cell (nnAPC) line, with adherent
CC blood monocytes and inoculating the subject with CD8+ suspension. The

```
CC   method is useful for treating cancer e.g. ovarian cancer, breast cancer
CC   and melanoma etc. It is also useful in cell therapy. The present sequence
CC   is human leukocyte antigen A2 (HLA-A2).1 restricted peptide epitope used
CC   to treat breast and ovarian cancer
XX
SQ   Sequence 10 AA;

  Query Match             100.0%;  Score 51;  DB 5;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.013;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db          1 VMAGVGSPYV 10


RESULT 11
AEA36306
ID   AEA36306 standard; peptide; 10 AA.
XX
AC   AEA36306;
XX
DT   11-AUG-2005  (first entry)
XX
DE   Human HER-2/neu 773-782 cytotoxic T-lymphocyte epitope peptide.
XX
KW   viral infection; virucide; cytostatic; tumor; neoplasm; cell therapy;
KW   antigen; HER-2/neu.
XX
OS   Homo sapiens.
XX
PN   JP2005139118-A.
XX
PD   02-JUN-2005.
XX
PF   07-NOV-2003; 2003JP-00377653.
XX
PR   20-FEB-2001; 2001US-0270252P.
XX
PA   (ORTH ) ORTHO-MCNEIL PHARM INC.
XX
PI   Leturco DJ,  Moriarty AM,  Jackson MR,  Peterson PA,  Richards JM;
XX
DR   WPI; 2002-667033/71.
XX
PT   Treating a subject with cancer comprises combining the CD+8 cells, which
PT   are stimulated with non-naturally occurring antigen-presenting cell line,
PT   with adherent blood monocytes and inoculating the subject with CD8+
PT   suspension.
XX
PS   Example 3; SEQ ID NO 16; 65pp; Japanese.
XX
CC   The invention relates to a novel method for treating viral infection in a
CC   subject. The method comprises preparing an antigen presentation cell
CC   lineage (nnAPC), collecting CD8+ cells from the subject, stimulating CD8+
CC   cells using the nnAPC, culturing CD8+ cells in the presence of
CC   interleukin-2 (IL-2) and/or IL-7, mixing peripheral blood monocytes from
CC   the subject, subjecting the components to gamma irradiation, combining
CC   the CD8+ cells with adhesive peripheral blood monocytes and inoculating
CC   the CD8+ suspended solid to the subject. The method of the invention
CC   demonstrates virucide and cytostatic activities and may be useful for
CC   treating a viral infection or tumor in a subject via cell therapy. The
CC   current sequence is that of a human HER-2/neu cytotoxic T-lymphocyte
CC   epitope peptide of the invention which was incorporated into a Drosophila
CC   antigen presenting cell.
XX
SQ   Sequence 10 AA;

  Query Match             100.0%;  Score 51;  DB 5;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.013;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db          1 VMAGVGSPYV 10


RESULT 12
ABU63012
ID   ABU63012 standard; peptide; 10 AA.
XX
AC   ABU63012;
XX
DT   16-SEP-2003  (first entry)
XX
DE   Human Her-2/Neu-derived CTL epitope HER-7.
XX
KW   CTL; cytotoxic C lymphocyte; epitope; p53; cytostatic; anti-tumour;
KW   virucide; immunosuppressive; vaccine; human; immune response;
KW   tumour-associated antigen; cancer; tumour; neoplasm; viral infection;
KW   retroviral infection; autoimmune response; Her-2; Neu.
XX
OS   Homo sapiens.
XX
PN   US2003064916-A1.
XX
PD   03-APR-2003.
XX
PF   26-MAR-1999;   99US-00277064.
XX
PR   08-AUG-1997;   97US-00860232.
XX
PA   (SHER/) SHERMAN L A.
XX
PI   Sherman LA;
XX
DR   WPI; 2003-512514/48.
XX
PT   Novel polypeptide useful for activating cytotoxic T lymphocytes in vivo
PT   which are useful in the diagnosis and treatment of variety of disease
PT   conditions such as cancer, tumors, and neoplasia.
XX
PS   Claim 5; Page 52; 77pp; English.
XX
CC   The invention relates to a polypeptide capable of specifically activating
CC   cytotoxic T lymphocytes (CTLs) in vivo which can then specifically target
CC   malignant cells, or having substantial homology with a CTL epitope, or
CC   its sequential subsets. Also included are a population of specific
CC   cytotoxic T cells capable of lysing tumour cells displaying a specific
CC   peptide, a vaccine comprising an immunogenically effective amount of CTL-
CC   stimulating peptide, generating activated CTL cells in vivo, generating
CC   CTL cells that will target a specific population of cells, specifically
CC   killing target cells in an individual using specific, activated CTLs,
CC   provoking an immune response to a tumour-associated antigen, identifying
CC   specific CTLs responsive to a specific T cell epitope, detecting specific
CC   CTLs having receptors capable of binding a specific T cell epitope in a
CC   tissue sample, detecting anti-p53 antibodies in an individual, an
CC   antibody molecule that immunoreacts with the polypeptide and a hybridoma
CC   capable of secreting the above antibodies. The methods are useful for
CC   specifically killing target cells in an individual using specific,
CC   activated CTLs and the polypeptide is useful for provoking an immune
CC   response to a tumour-associated antigen in mammal and the reaction occurs
CC   in vitro. The CTL epitope peptide is useful for activating CTLs in vivo
CC   with specificity for particular antigenic peptides, and these activated
CC   CTLs are useful in the diagnosis and treatment of variety of disease
CC   conditions such as cancer, tumours, neoplasia, viral and retroviral
CC   infections, and autoimmune response. The present sequence is a CTL
CC   epitope of the invention derived from the tumour associated antigen Her-
CC   2/Neu
XX
SQ   Sequence 10 AA;

  Query Match             100.0%;  Score 51;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.013;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

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Qy          1 VMAGVGSPYV 10
              ||||||||||
Db          1 VMAGVGSPYV 10
```

RESULT 13
ADE97756
ID ADE97756 standard; peptide; 10 AA.
XX
AC ADE97756;
XX
DT 12-FEB-2004 (first entry)
XX
DE Immunogenic HLA-A2.1 binding peptide #238.
XX
KW cytostatic; anti-inflammatory; hepatotropic; virucide; anti-HIV;
KW nephrotropic; neuroprotective; antiarthritic; antirheumatic;
KW immunosuppressive; dermatological; muscular; nephrotropic; thyromimetic;
KW haemostatic; antithyroid; antianaemic; anabolic; hypertensive;
KW immunogenic peptide composition; immune response; prostate cancer;
KW hepatitis B; hepatitis C; AIDS; renal carcinoma; cervical carcinoma;
KW lymphoma; cytomegalovirus; CMV; condlylloma acuminatum;
KW autoimmune associated disorder; multiple sclerosis; rheumatoid arthritis;
KW Sjogren syndrome; scleroderma; polymyositis; dermatomyositis;
KW systemic lupus erythematosus; juvenile rheumatoid arthritis;
KW ankylosing spondylitis; myasthenia gravis; MG; bullous pemphigoid;
KW pemphigus; glomerulonephritis; Goodpasture's syndrome;
KW autoimmune haemolytic anaemia; Hashimoto's disease; pernicious anaemia;
KW idiopathic thrombocytopenic purpura; Grave's disease; Addison's disease;
KW human leukocyte anitgen A2.1; HLA A2.1;
KW immunogenic HLA-A2.1 binding peptide.
XX
OS Synthetic.
XX
PN US2003185822-A1. — cannot be used as 102(e) bcc.
XX
PD 02-OCT-2003.
XX
PF 03-APR-2002; 2002US-00116557.
XX
PR 05-MAR-1993; 93US-00027146.
PR 04-JUN-1993; 93US-00073205.
PR 29-NOV-1993; 93US-00159184.
PR 02-DEC-1994; 94US-00349177.
XX
PA (GREY/) GREY H M.
PA (SETT/) SETTE A.
PA (SIDN/) SIDNEY J.
XX
PI Grey HM, Sette A, Sidney J;
XX
DR WPI; 2004-041186/04.
XX
PT Immunogenic peptide composition for preventing, treating or diagnosing
PT pathological states, e.g. prostate cancer, hepatitis B and C, Acquired
PT Immunodeficiency Syndrome, and renal carcinoma, includes conserved
PT residues at specified positions.
XX
PS Example 11; Page 25; 38pp; English.
XX
CC The invention describes an immunogenic peptide composition comprising 9
CC residues including a first conserved residue at a second position from N-
CC terminus, and a second conserved residue at C-terminal position. The
CC inventive peptide composition is used to elicit an immune response
CC against a desired antigen for preventing, treating or diagnosing
CC pathological states, e.g. prostate cancer, hepatitis B, hepatitis C,
CC AIDS, renal carcinoma, cervical carcinoma, lymphoma, cytomegalovirus
CC (CMV), and condlylloma acuminatum. It is also used to treat autoimmune
CC associated disorders, e.g. multiple sclerosis, rheumatoid arthritis,
CC Sjogren syndrome, scleroderma, polymyositis, dermatomyositis, systemic
CC lupus erythematosus, juvenile rheumatoid arthritis, ankylosing
CC spondylitis, myasthenia gravis (MG), bullous pemphigoid, pemphigus,
CC glomerulonephritis, Goodpasture's syndrome, autoimmune hemolytic anemia,
CC Hashimoto's disease, pernicious anaemia, idiopathic thrombocytopenic
CC purpura, Grave's disease, and Addison's disease. The invention defines
CC positions within a motif enabling the selection of the peptides, which
CC will bind efficiently to human leukocyte anitgen (HLA) A2.1. This is the
CC amino acid sequence of an immunogenic HLA-A2.1 binding peptide.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 51; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 VMAGVGSPYV 10
              ||||||||||
Db          1 VMAGVGSPYV 10
```

RESULT 14
ADM12647
ID ADM12647 standard; peptide; 10 AA.
XX
AC ADM12647;
XX
DT 20-MAY-2004 (first entry)
XX
DE MHC class I epitope of human Her-2/neu, 16-6-9.
XX
KW antigen presentation enhancing hybrid polypeptide; mammalian Ii-Key;
KW MHC class II; antibacterial; virucide; fungicide; antirheumatic;
KW antiarthritic; neuroprotective; dermatological; immunosuppressive;
KW antiinflammatory; antidiabetic; antithyroid; immune;
KW rheumatoid arthritis; multiple sclerosis; lupus erythematosus;
KW diabetes mellitus; myasthenia gravis; autoimmune thyroiditis;
KW scleroderma; dermatomyositis; pemphigus.
XX
OS Homo sapiens.
XX
PN US2003235594-A1.
XX
PD 25-DEC-2003.
XX
PF 17-SEP-2002; 2002US-00245871.
XX
PR 14-SEP-1999; 99US-00396813.
PR 17-JUL-2002; 2002US-00197000.
XX
PA (ANTI-) ANTIGEN EXPRESS INC.
XX
PI Humphreys R, Xu M;
XX
DR WPI; 2004-070554/07.
XX
PT Novel Ii-Key/antigen presentation enhancing hybrid polypeptide, useful
PT for treating infections, rheumatoid arthritis, multiple sclerosis, lupus
PT erythematosus and diabetes mellitus.
XX
PS Example 16; Page 55; 87pp; English.
XX
CC The invention relates to a novel antigen presentation enhancing hybrid
CC polypeptide. The novel polypeptide has an N-terminal element consisting
CC of 4-16 residues of a mammalian Ii-Key peptide and its non-N-terminal
CC deletion modifications, a chemical structure covalently linking the N-
CC terminal elelment to an MHC class II-presented epitope of a C-terminal
CC element. The C-terminal element comprises an antigenic epitope, which
CC binds to an antigenic peptide binding site of an MHC class II molecule.
CC The antigen presentation enhancing hybrid polypeptide has the following
CC activities: antibacterial, virucide, fungicide, antirheumatic,
CC antiarthritic, neuroprotective, dermatological, immunosuppressive,
CC antiinflammatory, antidiabetic, and antithyroid. The antigen presentation
CC enhancing hybrid polypeptide is useful for modulating the immune response
CC in an individual and for treating infections (such as bacteria, virus,
CC parasite and fungus), rheumatoid arthritis, multiple sclerosis, lupus
CC erythematosus, diabetes mellitus, myasthenia gravis, autoimmune

CC thyroiditis, scleroderma, dermatomyositis and pemphigus. This sequence
CC represents a mammalian Ii key related peptide epitope of the invention.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 51; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VMAGVGSPYV 10
||||||||||
Db 1 VMAGVGSPYV 10

RESULT 15
ADO38880
ID ADO38880 standard; peptide; 10 AA.
XX
AC ADO38880;
XX
DT 15-JUL-2004 (first entry)
XX
DE Human Her-2/neu MHC class II-presented epitope #67.
XX
KW Antibacterial; Virucide; Fungicide; Antiparasitic; Antiarthritic;
KW Antirheumatic; Neuroprotective; Antiinflammatory; Dermatological;
KW Immunosuppressive; Antidiabetic; Antithyroid; Antiasthmatic;
KW Antiallergic; Cytostatic; Antipsoriatic; Gene Therapy; Vaccine;
KW MHC Class II; Ii-key motif; immune response; anthrax; EBOLA; HIV;
KW influenza; vaccinia virus; infection; bacterium; virus; parasite; fungus;
KW rickettsia; rheumatoid arthritis; multiple sclerosis;
KW lupus erythematosus; diabetes mellitus; myasthenia gravis;
KW autoimmune thyroiditis; scleroderma; dermatomyositis; pemphigus; asthma;
KW allergic rhinitis; topical dermatitis; colitis; cancer; psoriasis;
KW adenoma.
XX
OS Homo sapiens.
XX
PN US2004058881-A1.
XX
PD 25-MAR-2004.
XX
PF 24-SEP-2002; 2002US-00253286.
XX
PR 24-SEP-2002; 2002US-00253286.
XX
PA (ANTI-) ANTIGEN EXPRESS INC.
XX
PI Humphreys RE, Xu M;
XX
DR WPI; 2004-294259/27.
XX
PT New non-naturally occurring protein or polypeptide modified by
PT recombinant DNA techniques, useful for treating multiple sclerosis,
PT diabetes mellitus, myasthenia gravis, scleroderma, allergic rhinitis,
PT colitis, cancer or psoriasis.
XX
PS Example 16; Page 57; 90pp; English.
XX
CC The invention relates to a non-naturally occurring protein or polypeptide
CC (I) modified by recombinant DNA techniques comprising: a C-terminal
CC element comprising an MHC Class II-presented epitope; an N-terminal
CC element comprising an Ii-key motif; and an intervening element comprising
CC a sequence of 4-11 amino acid residues where the modification by
CC recombinant DNA techniques taking place within elements (b) and (c). Also
CC described are methods for: suppressing or enhancing an immune response
CC directed toward an MHC (major histocompatibility complex) Class II-
CC presented epitope of interest. Suppressing an immune response directed
CC toward an MHC Class II-presented epitope of interest comprises: providing
CC a nucleic acid sequence encoding the MHC Class II-presented epitope of
CC interest, the nucleic acid sequence encoding an Ii-Key motif located 4-11
CC amino acids upstream from the N-terminal residue of the MHC Class II-
CC presented epitope of interest; and modifying the Ii-Key motif to decrease
CC its conformance to the archetypal Ii-Key regulatory motif. Enhancing an
CC immune response directed toward an MHC Class II-presented epitope of
CC interest comprises: providing a nucleic acid sequence encoding the MHC
CC Class II-presented epitope of interest, the nucleic acid sequence lacking
CC an Ii-key motif located 4-11 amino acids upstream from the N-terminal
CC residue of the MHC Class II-presented epitope of interest; and modifying
CC the nucleic acid sequence to introduce an Ii-key motif appropriately
CC spaced from the MHC Class II-presented epitope. The protein or
CC polypeptide of interest corresponds to a protein or polypeptide encoded
CC by an infectious pathogen selected from anthrax, EBOLA, HIV or influenza,
CC preferably vaccinia virus. The non-naturally occurring protein or
CC polypeptide (I) modified by recombinant DNA techniques is useful for
CC treating infectious diseases caused or associated with infection by a
CC bacterium, virus, parasite, fungus, rickettsia or other infectious
CC agents. It is also useful for treating rheumatoid arthritis, multiple
CC sclerosis, lupus erythematosus, diabetes mellitus, myasthenia gravis,
CC autoimmune thyroiditis, scleroderma, dermatomyositis, pemphigus, asthma,
CC allergic rhinitis, topical dermatitis, colitis, cancer, psoriasis or
CC adenomas. The present sequence represents the amino acid sequence of an
CC MHC class II-presented epitope used in the invention.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 51; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VMAGVGSPYV 10
||||||||||
Db 1 VMAGVGSPYV 10

Search completed: April 11, 2006, 19:30:43
Job time : 190 secs

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OM protein - protein search, using sw model

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Perfect score: 51
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Total number of hits satisfying chosen parameters: 48921

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	51	100.0	10	7	US-11-033-039-620	Sequence 620, App
2	41	80.4	9	6	US-10-510-101-135	Sequence 135, App
3	29	56.9	9	7	US-11-045-024-2492	Sequence 2492, Ap
4	29	56.9	9	7	US-11-045-024-7995	Sequence 7995, Ap
5	29	56.9	10	7	US-11-045-024-2498	Sequence 2498, Ap
6	29	56.9	10	7	US-11-045-024-4891	Sequence 4891, Ap
7	29	56.9	10	7	US-11-045-024-6819	Sequence 6819, Ap
8	26	51.0	9	6	US-10-966-483-5	Sequence 5, Appli
9	26	51.0	9	6	US-10-511-273-7	Sequence 7, Appli
10	24	47.1	9	6	US-10-517-784-42	Sequence 42, Appl
11	24	47.1	10	7	US-11-125-837-12	Sequence 12, Appl
12	23	45.1	8	7	US-11-045-024-2949	Sequence 2949, Ap
13	23	45.1	8	7	US-11-045-024-2950	Sequence 2950, Ap
14	23	45.1	8	7	US-11-045-024-9135	Sequence 9135, Ap
15	23	45.1	8	7	US-11-045-024-9136	Sequence 9136, Ap
16	23	45.1	8	7	US-11-045-024-9240	Sequence 9240, Ap
17	23	45.1	8	7	US-11-045-024-9252	Sequence 9252, Ap
18	23	45.1	8	7	US-11-045-024-11312	Sequence 11312, A
19	23	45.1	8	7	US-11-045-024-11313	Sequence 11313, A
20	23	45.1	8	7	US-11-045-024-11376	Sequence 11376, A
21	23	45.1	8	7	US-11-045-024-11383	Sequence 11383, A
22	23	45.1	9	7	US-11-021-441-67	Sequence 67, Appl
23	23	45.1	9	7	US-11-045-024-1234	Sequence 1234, Ap
24	23	45.1	9	7	US-11-045-024-1235	Sequence 1235, Ap
25	23	45.1	9	7	US-11-045-024-9139	Sequence 9139, Ap
26	23	45.1	9	7	US-11-045-024-9140	Sequence 9140, Ap
27	23	45.1	9	7	US-11-045-024-9242	Sequence 9242, Ap
28	23	45.1	9	7	US-11-045-024-9255	Sequence 9255, Ap
29	23	45.1	9	7	US-11-045-024-11315	Sequence 11315, A
30	23	45.1	9	7	US-11-045-024-11377	Sequence 11377, A
31	23	45.1	9	7	US-11-033-039-467	Sequence 467, App
32	23	45.1	10	7	US-11-045-024-3016	Sequence 3016, Ap
33	23	45.1	10	7	US-11-045-024-3017	Sequence 3017, Ap
34	23	45.1	10	7	US-11-045-024-9127	Sequence 9127, Ap
35	23	45.1	10	7	US-11-045-024-9142	Sequence 9142, Ap
36	23	45.1	10	7	US-11-045-024-9143	Sequence 9143, Ap
37	23	45.1	10	7	US-11-045-024-9244	Sequence 9244, Ap
38	23	45.1	10	7	US-11-045-024-9245	Sequence 9245, Ap
39	23	45.1	10	7	US-11-045-024-9257	Sequence 9257, Ap
40	23	45.1	10	7	US-11-045-024-11306	Sequence 11306, A
41	23	45.1	10	7	US-11-045-024-11317	Sequence 11317, A
42	23	45.1	10	7	US-11-045-024-11378	Sequence 11378, A
43	23	45.1	10	7	US-11-045-024-11386	Sequence 11386, A
44	22	43.1	6	7	US-11-032-773-743	Sequence 743, App
45	22	43.1	6	7	US-11-197-315-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-11-033-039-620
; Sequence 620, Application US/11033039
; Publication No. US20060002947A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2017US01
; CURRENT APPLICATION NUMBER: US/11/033,039
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 10/245,871
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 620
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-033-039-620

Query Match 100.0%; Score 51; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00065;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VMAGVGSPYV 10
||||||||||
Db 1 VMAGVGSPYV 10

RESULT 2
US-10-510-101-135
; Sequence 135, Application US/10510101
; Publication No. US20060018915A1
; GENERAL INFORMATION:
; APPLICANT: Epimmune Inc.
; APPLICANT: Ishioka, Glenn
; APPLICANT: Fikes, John
; APPLICANT: Tangri, Shabnam
; APPLICANT: Sette, Alessandro
; TITLE OF INVENTION: Heteroclitic Analogs and Related Methods
; FILE REFERENCE: 2060.009PC05
; CURRENT APPLICATION NUMBER: US/10/510,101
; CURRENT FILING DATE: 2004-10-05

```
;  PRIOR APPLICATION NUMBER: US 60/413,471
;  PRIOR FILING DATE: 2002-09-26
;  PRIOR APPLICATION NUMBER: US 10/116,118
;  PRIOR FILING DATE: 2002-04-05
;  NUMBER OF SEQ ID NOS: 196
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 135
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic peptide derived from Homo sapiens Her2/neu
US-10-510-101-135

  Query Match             80.4%;  Score 41;  DB 6;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.4e+05;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPY 9
              || ||||||
Db          1 VMDGVGSPY 9


RESULT 3
US-11-045-024-2492
; Sequence 2492, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
;  APPLICANT: Sette, Alessandro
;  APPLICANT:  Sidney,John
;  APPLICANT:  Southwood, Scott
;  APPLICANT:  Livingston, Brian
;  APPLICANT:  Chesnut, Robert
;  APPLICANT:  Baker, Denise Marie
;  APPLICANT:  Celis, Esteban
;  APPLICANT:  Kubo, Ralph
;  APPLICANT:  Grey, Howard M.
;  APPLICANT:  Epimmune Inc.
;  TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
;  TITLE OF INVENTION:  Virus-1 Using Peptide and Nucleic Acid Compositions
;  FILE REFERENCE: 2060.0040007
;  CURRENT APPLICATION NUMBER: US/11/045,024
;  CURRENT FILING DATE:  2005-01-28
;  PRIOR APPLICATION NUMBER: US 09/412,863
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: US 08/027,146
;  PRIOR FILING DATE: 1993-03-05
;  PRIOR APPLICATION NUMBER: US 08/073,205
;  PRIOR FILING DATE: 1993-06-04
;  PRIOR APPLICATION NUMBER: US 08/103,396
;  PRIOR FILING DATE: 1993-08-06
;  PRIOR APPLICATION NUMBER: US 08/159,184
;  PRIOR FILING DATE: 1993-11-29
;  PRIOR APPLICATION NUMBER: US 08/159,339
;  PRIOR FILING DATE: 1993-11-29
;  PRIOR APPLICATION NUMBER: US 08/205,713
;  PRIOR FILING DATE: 1994-03-04
;  PRIOR APPLICATION NUMBER: US 08/347,610
;  PRIOR FILING DATE: 1994-12-01
;  NUMBER OF SEQ ID NOS: 14528
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2492
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-2492

  Query Match             56.9%;  Score 29;  DB 7;  Length 9;
  Best Local Similarity   71.4%;  Pred. No. 1.4e+05;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 GVGSPYV 10
              ||||| :
Db          3 GVGSPQI 9


RESULT 4
US-11-045-024-7995
; Sequence 7995, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
;  APPLICANT: Sette, Alessandro
;  APPLICANT:  Sidney,John
;  APPLICANT:  Southwood, Scott
;  APPLICANT:  Livingston, Brian
;  APPLICANT:  Chesnut, Robert
;  APPLICANT:  Baker, Denise Marie
;  APPLICANT:  Celis, Esteban
;  APPLICANT:  Kubo, Ralph
;  APPLICANT:  Grey, Howard M.
;  APPLICANT:  Epimmune Inc.
;  TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
;  TITLE OF INVENTION:  Virus-1 Using Peptide and Nucleic Acid Compositions
;  FILE REFERENCE: 2060.0040007
;  CURRENT APPLICATION NUMBER: US/11/045,024
;  CURRENT FILING DATE:  2005-01-28
;  PRIOR APPLICATION NUMBER: US 09/412,863
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: US 08/027,146
;  PRIOR FILING DATE: 1993-03-05
;  PRIOR APPLICATION NUMBER: US 08/073,205
;  PRIOR FILING DATE: 1993-06-04
;  PRIOR APPLICATION NUMBER: US 08/103,396
;  PRIOR FILING DATE: 1993-08-06
;  PRIOR APPLICATION NUMBER: US 08/159,184
;  PRIOR FILING DATE: 1993-11-29
;  PRIOR APPLICATION NUMBER: US 08/159,339
;  PRIOR FILING DATE: 1993-11-29
;  PRIOR APPLICATION NUMBER: US 08/205,713
;  PRIOR FILING DATE: 1994-03-04
;  PRIOR APPLICATION NUMBER: US 08/347,610
;  PRIOR FILING DATE: 1994-12-01
;  NUMBER OF SEQ ID NOS: 14528
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7995
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-7995

  Query Match             56.9%;  Score 29;  DB 7;  Length 9;
  Best Local Similarity   71.4%;  Pred. No. 1.4e+05;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 GVGSPYV 10
              ||||| :
Db          3 GVGSPQI 9


RESULT 5
US-11-045-024-2498
; Sequence 2498, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
;  APPLICANT: Sette, Alessandro
;  APPLICANT:  Sidney,John
;  APPLICANT:  Southwood, Scott
;  APPLICANT:  Livingston, Brian
;  APPLICANT:  Chesnut, Robert
;  APPLICANT:  Baker, Denise Marie
;  APPLICANT:  Celis, Esteban
;  APPLICANT:  Kubo, Ralph
;  APPLICANT:  Grey, Howard M.
;  APPLICANT:  Epimmune Inc.
;  TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
;  TITLE OF INVENTION:  Virus-1 Using Peptide and Nucleic Acid Compositions
```

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;  FILE REFERENCE: 2060.0040007
;  CURRENT APPLICATION NUMBER: US/11/045,024
;  CURRENT FILING DATE:  2005-01-28
;  PRIOR APPLICATION NUMBER: US 09/412,863
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: US 08/027,146
;  PRIOR FILING DATE: 1993-03-05
;  PRIOR APPLICATION NUMBER: US 08/073,205
;  PRIOR FILING DATE: 1993-06-04
;  PRIOR APPLICATION NUMBER: US 08/103,396
;  PRIOR FILING DATE: 1993-08-06
;  PRIOR APPLICATION NUMBER: US 08/159,184
;  PRIOR FILING DATE: 1993-11-29
;  PRIOR APPLICATION NUMBER: US 08/159,339
;  PRIOR FILING DATE: 1993-11-29
;  PRIOR APPLICATION NUMBER: US 08/205,713
;  PRIOR FILING DATE: 1994-03-04
;  PRIOR APPLICATION NUMBER: US 08/347,610
;  PRIOR FILING DATE: 1994-12-01
;  NUMBER OF SEQ ID NOS: 14528
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2498
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-2498

  Query Match             56.9%;  Score 29;  DB 7;  Length 10;
  Best Local Similarity   71.4%;  Pred. No. 10;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 GVGSPYV 10
              ||||| :
Db          4 GVGSPQI 10


RESULT 6
US-11-045-024-4891
; Sequence 4891, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
;  APPLICANT: Sette, Alessandro
;  APPLICANT:  Sidney,John
;  APPLICANT:  Southwood, Scott
;  APPLICANT:  Livingston, Brian
;  APPLICANT:  Chesnut, Robert
;  APPLICANT:  Baker, Denise Marie
;  APPLICANT:  Celis, Esteban
;  APPLICANT:  Kubo, Ralph
;  APPLICANT:  Grey, Howard M.
;  APPLICANT:  Epimmune Inc.
;  TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
;  TITLE OF INVENTION:  Virus-1 Using Peptide and Nucleic Acid Compositions
;  FILE REFERENCE: 2060.0040007
;  CURRENT APPLICATION NUMBER: US/11/045,024
;  CURRENT FILING DATE:  2005-01-28
;  PRIOR APPLICATION NUMBER: US 09/412,863
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: US 08/027,146
;  PRIOR FILING DATE: 1993-03-05
;  PRIOR APPLICATION NUMBER: US 08/073,205
;  PRIOR FILING DATE: 1993-06-04
;  PRIOR APPLICATION NUMBER: US 08/103,396
;  PRIOR FILING DATE: 1993-08-06
;  PRIOR APPLICATION NUMBER: US 08/159,184
;  PRIOR FILING DATE: 1993-11-29
;  PRIOR APPLICATION NUMBER: US 08/159,339
;  PRIOR FILING DATE: 1993-11-29
;  PRIOR APPLICATION NUMBER: US 08/205,713
;  PRIOR FILING DATE: 1994-03-04
;  PRIOR APPLICATION NUMBER: US 08/347,610
;  PRIOR FILING DATE: 1994-12-01
;  NUMBER OF SEQ ID NOS: 14528
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4891
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-4891

  Query Match             56.9%;  Score 29;  DB 7;  Length 10;
  Best Local Similarity   71.4%;  Pred. No. 10;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 GVGSPYV 10
              ||||| :
Db          4 GVGSPQI 10


RESULT 7
US-11-045-024-6819
; Sequence 6819, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
;  APPLICANT: Sette, Alessandro
;  APPLICANT:  Sidney,John
;  APPLICANT:  Southwood, Scott
;  APPLICANT:  Livingston, Brian
;  APPLICANT:  Chesnut, Robert
;  APPLICANT:  Baker, Denise Marie
;  APPLICANT:  Celis, Esteban
;  APPLICANT:  Kubo, Ralph
;  APPLICANT:  Grey, Howard M.
;  APPLICANT:  Epimmune Inc.
;  TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
;  TITLE OF INVENTION:  Virus-1 Using Peptide and Nucleic Acid Compositions
;  FILE REFERENCE: 2060.0040007
;  CURRENT APPLICATION NUMBER: US/11/045,024
;  CURRENT FILING DATE:  2005-01-28
;  PRIOR APPLICATION NUMBER: US 09/412,863
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: US 08/027,146
;  PRIOR FILING DATE: 1993-03-05
;  PRIOR APPLICATION NUMBER: US 08/073,205
;  PRIOR FILING DATE: 1993-06-04
;  PRIOR APPLICATION NUMBER: US 08/103,396
;  PRIOR FILING DATE: 1993-08-06
;  PRIOR APPLICATION NUMBER: US 08/159,184
;  PRIOR FILING DATE: 1993-11-29
;  PRIOR APPLICATION NUMBER: US 08/159,339
;  PRIOR FILING DATE: 1993-11-29
;  PRIOR APPLICATION NUMBER: US 08/205,713
;  PRIOR FILING DATE: 1994-03-04
;  PRIOR APPLICATION NUMBER: US 08/347,610
;  PRIOR FILING DATE: 1994-12-01
;  NUMBER OF SEQ ID NOS: 14528
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6819
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-6819

  Query Match             56.9%;  Score 29;  DB 7;  Length 10;
  Best Local Similarity   71.4%;  Pred. No. 10;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 GVGSPYV 10
              ||||| :
Db          4 GVGSPQI 10


RESULT 8
US-10-966-483-5
; Sequence 5, Application US/10966483
; Publication No. US20050281783A1
```

```
; GENERAL INFORMATION:
;  APPLICANT: Kinch, Michael S.
;  APPLICANT:  Kiener, Peter A.
;  APPLICANT:  Bruckheimer, Elizabeth
;  APPLICANT:  Dubensky, Jr. Thomas W.
;  APPLICANT:  Cook, David N.
;  TITLE OF INVENTION: LISTERIA-BASED EphA2 VACCINES
;  FILE REFERENCE: 10271-146
;  CURRENT APPLICATION NUMBER: US/10/966,483
;  CURRENT FILING DATE:  2004-10-15
;  PRIOR APPLICATION NUMBER: US 60/511,919
;  PRIOR FILING DATE: 2003-10-15
;  PRIOR APPLICATION NUMBER: US 60/511,719
;  PRIOR FILING DATE: 2003-10-15
;  PRIOR APPLICATION NUMBER: US 60/532,666
;  PRIOR FILING DATE: 2003-12-24
;  PRIOR APPLICATION NUMBER: US 60/556,631
;  PRIOR FILING DATE: 2004-03-26
;  PRIOR APPLICATION NUMBER:
;  PRIOR FILING DATE: 2004-10-01
;  PRIOR APPLICATION NUMBER:
;  PRIOR FILING DATE: 2004-10-07
;  NUMBER OF SEQ ID NOS: 72
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-966-483-5

  Query Match           51.0%;  Score 26;  DB 6;  Length 9;
  Best Local Similarity  83.3%;  Pred. No. 1.4e+05;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVG 6
              |:||||
Db          1 VLAGVG 6


RESULT 9
US-10-511-273-7
; Sequence 7, Application US/10511273
; Publication No. US20060034856A1
; GENERAL INFORMATION:
;  APPLICANT: KOSMATOPOULOS, KOSTAS
;  APPLICANT:  ALVES, PEDRO
;  TITLE OF INVENTION: EPHA2 ANTIGEN T EPITOPES
;  FILE REFERENCE: 260449US0XPCT
;  CURRENT APPLICATION NUMBER: US/10/511,273
;  CURRENT FILING DATE:  2004-10-21
;  PRIOR APPLICATION NUMBER: PCT/FR03/01280
;  PRIOR FILING DATE: 2003-04-23
;  PRIOR APPLICATION NUMBER: FR 02/05048
;  PRIOR FILING DATE: 2002-04-23
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Peptide
US-10-511-273-7

  Query Match           51.0%;  Score 26;  DB 6;  Length 9;
  Best Local Similarity  83.3%;  Pred. No. 1.4e+05;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVG 6
              |:||||
Db          1 VLAGVG 6


RESULT 10
US-10-517-784-42
; Sequence 42, Application US/10517784
; Publication No. US20060003315A1
; GENERAL INFORMATION:
;  APPLICANT: GROSS, Gideon
;  APPLICANT:  MARGALIT, Alon
;  TITLE OF INVENTION: MEMBRANE-ANCHORED BETA-2 MICROGLOBULIN COVALENTLY LINKED TO MHC
;  TITLE OF INVENTION:  PEPTIDE EPITOPES
;  FILE REFERENCE: GAVISH-004 US
;  CURRENT APPLICATION NUMBER: US/10/517,784
;  CURRENT FILING DATE:  2004-12-13
;  PRIOR APPLICATION NUMBER: US 60/388,273
;  PRIOR FILING DATE: 2002-06-12
;  PRIOR APPLICATION NUMBER: PCT/IL03/00501
;  PRIOR FILING DATE: 2003-06-12
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-10-517-784-42

  Query Match           47.1%;  Score 24;  DB 6;  Length 9;
  Best Local Similarity  50.0%;  Pred. No. 1.4e+05;
  Matches    4;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 MAGVGSPY 9
              : | | ||
Db          1 LLGPGRPY 8


RESULT 11
US-11-125-837-12
; Sequence 12, Application US/11125837
; Publication No. US20050266003A1
; GENERAL INFORMATION:
;  APPLICANT: Lin, Rong-Hwa
;  APPLICANT:  Chang, Chung Nan
;  APPLICANT:  Chen, Pei-Jiun
;  APPLICANT:  Huang, Chiu-Chen
;  TITLE OF INVENTION: ANTIBODIES
;  FILE REFERENCE: 13062-011001
;  CURRENT APPLICATION NUMBER: US/11/125,837
;  CURRENT FILING DATE:  2005-05-10
;  PRIOR APPLICATION NUMBER: US 60/569,892
;  PRIOR FILING DATE: 2004-05-10
;  NUMBER OF SEQ ID NOS: 100
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-11-125-837-12

  Query Match           47.1%;  Score 24;  DB 7;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 91;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GSPY 9
              ||||
Db          2 GSPY 5


RESULT 12
US-11-045-024-2949
; Sequence 2949, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
;  APPLICANT: Sette, Alessandro
```

```
;  APPLICANT:  Sidney,John
;  APPLICANT:  Southwood, Scott
;  APPLICANT:  Livingston, Brian
;  APPLICANT:  Chesnut, Robert
;  APPLICANT:  Baker, Denise Marie
;  APPLICANT:  Celis, Esteban
;  APPLICANT:  Kubo, Ralph
;  APPLICANT:  Grey, Howard M.
;  APPLICANT:  Epimmune Inc.
;  TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
;  TITLE OF INVENTION:  Virus-1 Using Peptide and Nucleic Acid Compositions
;  FILE REFERENCE: 2060.0040007
;  CURRENT APPLICATION NUMBER: US/11/045,024
;  CURRENT FILING DATE:  2005-01-28
;  PRIOR APPLICATION NUMBER: US 09/412,863
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: US 08/027,146
;  PRIOR FILING DATE: 1993-03-05
;  PRIOR APPLICATION NUMBER: US 08/073,205
;  PRIOR FILING DATE: 1993-06-04
;  PRIOR APPLICATION NUMBER: US 08/103,396
;  PRIOR FILING DATE: 1993-08-06
;  PRIOR APPLICATION NUMBER: US 08/159,184
;  PRIOR FILING DATE: 1993-11-29
;  PRIOR APPLICATION NUMBER: US 08/159,339
;  PRIOR FILING DATE: 1993-11-29
;  PRIOR APPLICATION NUMBER: US 08/205,713
;  PRIOR FILING DATE: 1994-03-04
;  PRIOR APPLICATION NUMBER: US 08/347,610
;  PRIOR FILING DATE: 1994-12-01
;  NUMBER OF SEQ ID NOS: 14528
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2949
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-2949

  Query Match             45.1%;  Score 23;  DB 7;  Length 8;
  Best Local Similarity   80.0%;  Pred. No. 1.4e+05;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 GVGSP 8
              ||| |
Db          1 GVGGP 5


RESULT 13
US-11-045-024-2950
; Sequence 2950, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
;  APPLICANT: Sette, Alessandro
;  APPLICANT:  Sidney,John
;  APPLICANT:  Southwood, Scott
;  APPLICANT:  Livingston, Brian
;  APPLICANT:  Chesnut, Robert
;  APPLICANT:  Baker, Denise Marie
;  APPLICANT:  Celis, Esteban
;  APPLICANT:  Kubo, Ralph
;  APPLICANT:  Grey, Howard M.
;  APPLICANT:  Epimmune Inc.
;  TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
;  TITLE OF INVENTION:  Virus-1 Using Peptide and Nucleic Acid Compositions
;  FILE REFERENCE: 2060.0040007
;  CURRENT APPLICATION NUMBER: US/11/045,024
;  CURRENT FILING DATE:  2005-01-28
;  PRIOR APPLICATION NUMBER: US 09/412,863
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: US 08/027,146
;  PRIOR FILING DATE: 1993-03-05
;  PRIOR APPLICATION NUMBER: US 08/073,205
;  PRIOR FILING DATE: 1993-06-04
;  PRIOR APPLICATION NUMBER: US 08/103,396
;  PRIOR FILING DATE: 1993-08-06
;  PRIOR APPLICATION NUMBER: US 08/159,184
;  PRIOR FILING DATE: 1993-11-29
;  PRIOR APPLICATION NUMBER: US 08/159,339
;  PRIOR FILING DATE: 1993-11-29
;  PRIOR APPLICATION NUMBER: US 08/205,713
;  PRIOR FILING DATE: 1994-03-04
;  PRIOR APPLICATION NUMBER: US 08/347,610
;  PRIOR FILING DATE: 1994-12-01
;  NUMBER OF SEQ ID NOS: 14528
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2950
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-2950

  Query Match             45.1%;  Score 23;  DB 7;  Length 8;
  Best Local Similarity   80.0%;  Pred. No. 1.4e+05;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 GVGSP 8
              ||| |
Db          1 GVGGP 5


RESULT 14
US-11-045-024-9135
; Sequence 9135, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
;  APPLICANT: Sette, Alessandro
;  APPLICANT:  Sidney,John
;  APPLICANT:  Southwood, Scott
;  APPLICANT:  Livingston, Brian
;  APPLICANT:  Chesnut, Robert
;  APPLICANT:  Baker, Denise Marie
;  APPLICANT:  Celis, Esteban
;  APPLICANT:  Kubo, Ralph
;  APPLICANT:  Grey, Howard M.
;  APPLICANT:  Epimmune Inc.
;  TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
;  TITLE OF INVENTION:  Virus-1 Using Peptide and Nucleic Acid Compositions
;  FILE REFERENCE: 2060.0040007
;  CURRENT APPLICATION NUMBER: US/11/045,024
;  CURRENT FILING DATE:  2005-01-28
;  PRIOR APPLICATION NUMBER: US 09/412,863
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: US 08/027,146
;  PRIOR FILING DATE: 1993-03-05
;  PRIOR APPLICATION NUMBER: US 08/073,205
;  PRIOR FILING DATE: 1993-06-04
;  PRIOR APPLICATION NUMBER: US 08/103,396
;  PRIOR FILING DATE: 1993-08-06
;  PRIOR APPLICATION NUMBER: US 08/159,184
;  PRIOR FILING DATE: 1993-11-29
;  PRIOR APPLICATION NUMBER: US 08/159,339
;  PRIOR FILING DATE: 1993-11-29
;  PRIOR APPLICATION NUMBER: US 08/205,713
;  PRIOR FILING DATE: 1994-03-04
;  PRIOR APPLICATION NUMBER: US 08/347,610
;  PRIOR FILING DATE: 1994-12-01
;  NUMBER OF SEQ ID NOS: 14528
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9135
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-9135

  Query Match             45.1%;  Score 23;  DB 7;  Length 8;
  Best Local Similarity   80.0%;  Pred. No. 1.4e+05;
```

```
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 GVGSP 8
              ||| |
Db          2 GVGGP 6


RESULT 15
US-11-045-024-9136
; Sequence 9136, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
;  APPLICANT: Sette, Alessandro
;  APPLICANT:  Sidney,John
;  APPLICANT:  Southwood, Scott
;  APPLICANT:  Livingston, Brian
;  APPLICANT:  Chesnut, Robert
;  APPLICANT:  Baker, Denise Marie
;  APPLICANT:  Celis, Esteban
;  APPLICANT:  Kubo, Ralph
;  APPLICANT:  Grey, Howard M.
;  APPLICANT:  Epimmune Inc.
;  TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
;  TITLE OF INVENTION:  Virus-1 Using Peptide and Nucleic Acid Compositions
;  FILE REFERENCE: 2060.0040007
;  CURRENT APPLICATION NUMBER: US/11/045,024
;  CURRENT FILING DATE:  2005-01-28
;  PRIOR APPLICATION NUMBER: US 09/412,863
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: US 08/027,146
;  PRIOR FILING DATE: 1993-03-05
;  PRIOR APPLICATION NUMBER: US 08/073,205
;  PRIOR FILING DATE: 1993-06-04
;  PRIOR APPLICATION NUMBER: US 08/103,396
;  PRIOR FILING DATE: 1993-08-06
;  PRIOR APPLICATION NUMBER: US 08/159,184
;  PRIOR FILING DATE: 1993-11-29
;  PRIOR APPLICATION NUMBER: US 08/159,339
;  PRIOR FILING DATE: 1993-11-29
;  PRIOR APPLICATION NUMBER: US 08/205,713
;  PRIOR FILING DATE: 1994-03-04
;  PRIOR APPLICATION NUMBER: US 08/347,610
;  PRIOR FILING DATE: 1994-12-01
;  NUMBER OF SEQ ID NOS: 14528
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9136
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-9136

  Query Match             45.1%;  Score 23;  DB 7;  Length 8;
  Best Local Similarity   80.0%;  Pred. No. 1.4e+05;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 GVGSP 8
              ||| |
Db          1 GVGGP 5


Search completed: April 11, 2006, 19:27:28
Job time : 25 secs
```

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 11, 2006, 19:18:59 ; Search time 38 Seconds
(without alignments)
25.320 Million cell updates/sec

Title: US-09-277-064-12
Perfect score: 51
Sequence: 1 VMAGVGSPYV 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 1102

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	24	47.1	9	2	PH1591	Ig H chain V-D-J r
2	19	37.3	8	2	E47393	neuropeptide calla
3	18	35.3	7	2	T09512	NADH2 dehydrogenas
4	18	35.3	8	2	F60588	sperm-activating p
5	18	35.3	9	2	S65865	collagen alpha 2(V
6	17	33.3	5	2	A41225	copper resistance
7	17	33.3	6	2	A27696	contraction-inhibi
8	17	33.3	8	2	PT0627	T-cell receptor be
9	17	33.3	9	2	PT0324	Ig heavy chain CRD
10	17	33.3	10	2	C39111	Ig heavy chain C r
11	17	33.3	10	2	G60787	sperm-activating p
12	17	33.3	10	2	I60588	sperm-activating p
13	16	31.4	5	2	C23751	spinal cord peptid
14	16	31.4	7	2	PT0623	T-cell receptor be
15	16	31.4	8	2	PT0631	T-cell receptor be
16	16	31.4	8	2	G60588	sperm-activating p
17	16	31.4	10	2	PT0230	Ig heavy chain CDR
18	16	31.4	10	2	PH0927	T-cell receptor be
19	16	31.4	10	2	H60787	sperm-activating p
20	16	31.4	10	2	F60787	sperm-activating p
21	16	31.4	10	2	D60787	sperm-activating p
22	16	31.4	10	2	B60787	sperm-activating p
23	16	31.4	10	2	D60588	sperm-activating p
24	16	31.4	10	2	B60588	sperm-activating p
25	16	31.4	10	2	C60588	sperm-activating p
26	16	31.4	10	2	I60527	sperm-activating p
27	16	31.4	10	2	D60527	sperm-activating p
28	16	31.4	10	2	C39572	sperm-activating p
29	16	31.4	10	2	F60527	sperm-activating p
30	16	31.4	10	2	C60527	sperm-activating p
31	16	31.4	10	2	E60527	sperm-activating p
32	16	31.4	10	2	G60527	sperm-activating p
33	16	31.4	10	2	E39572	sperm-activating p
34	16	31.4	10	2	D60788	sperm-activating p
35	16	31.4	10	2	E60788	sperm-activating p
36	16	31.4	10	2	C60788	sperm-activating p
37	16	31.4	10	2	F60589	sperm-activating p
38	16	31.4	10	2	C60589	sperm-activating p
39	16	31.4	10	2	D60589	sperm-activating p
40	16	31.4	10	2	A60527	sperm-activating p
41	16	31.4	10	2	A60787	sperm-activating p
42	16	31.4	10	2	A60588	sperm-activating p
43	16	31.4	10	2	A60788	sperm-activating p
44	15	29.4	5	2	I40702	primase - Citrobac
45	15	29.4	6	2	I51434	H4 histone - Afric

ALIGNMENTS

RESULT 1
PH1591
Ig H chain V-D-J region (wild-type clone 142) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Accession: PH1591
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mic
A;Reference number: PH1580; MUID:93301609; PMID:8315387
A;Accession: PH1591
A;Molecule type: DNA
A;Residues: 1-9 <LEV>
A;Cross-references: UNIPARC:UPI000017C6B2
A;Experimental source: bone marrow pre-B lymphocyte
C;Keywords: immunoglobulin

Query Match 47.1%; Score 24; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          6 GSPY 9
              ||||
Db          4 GSPY 7
```

RESULT 2
E47393
neuropeptide callatostatin 5 - bluebottle fly (Calliphora vomitoria)
C;Species: Calliphora vomitoria
C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: E47393
R;Duve, H.; Johnsen, A.H.; Scott, A.G.; Yu, C.G.; Yagi, K.J.; Tobe, S.S.; Thorpe, A.
Proc. Natl. Acad. Sci. U.S.A. 90, 2456-2460, 1993
A;Title: Callatostatins: neuropeptides from the blowfly Calliphora vomitoria with seque
A;Reference number: A47393; MUID:93211980; PMID:8460157
A;Accession: E47393
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-8 <DUV>
A;Cross-references: UNIPROT:P41841; UNIPARC:UPI000002EAB5
A;Experimental source: whole flies
A;Note: sequence extracted from NCBI backbone (NCBIP:128482)

Query Match 37.3%; Score 19; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          6 GSPY 9
              | ||
Db          1 GPPY 4
```

```
RESULT 3
T09512
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - rape mitochondrion (fragment)
C;Species: mitochondrion Brassica napus (rape)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 03-Jun-2002
C;Accession: T09512
R;L'Homme, Y.
submitted to the EMBL Data Library, June 1994
A;Reference number: Z16706
A;Accession: T09512
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-7 <LHO>
A;Cross-references: UNIPARC:UPI000011E90B; EMBL:U10423; NID:g1800190; PID:g1800192
C;Genetics:
A;Gene: nad5
A;Genome: mitochondrion
C;Keywords: mitochondrion; NAD; oxidative phosphorylation; oxidoreductase; respiratory c

  Query Match             35.3%;  Score 18;  DB 2;  Length 7;
  Best Local Similarity   50.0%;  Pred. No. 2.8e+05;
  Matches    3;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VMAGVG 6
              :| |:|
Db          2 MMIGLG 7


RESULT 4
F60588
sperm-activating peptide b - sea urchin (Pseudoboletia maculata)
N;Alternate names: speract homolog
C;Species: Pseudoboletia maculata
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-2004
C;Accession: F60588
R;Yoshino, K.I.; Kajiura, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamaguc
Comp. Biochem. Physiol. B 94, 739-751, 1989
A;Title: A halogenated amino acid-containing sperm activating peptide and its related pe
otus nudus, Echinometra mathaei and Heterocentrotus mammillatus.
A;Reference number: A60527
A;Accession: F60588
A;Molecule type: protein
A;Residues: 1-8 <YOS>
A;Cross-references: UNIPARC:UPI000017A4DF

  Query Match             35.3%;  Score 18;  DB 2;  Length 8;
  Best Local Similarity   60.0%;  Pred. No. 2.8e+05;
  Matches    3;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 MAGVG 6
              : |||
Db          4 LXGVG 8


RESULT 5
S65865
collagen alpha 2(V) chain - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 29-Aug-1997
C;Accession: S65865
R;Niyibizi, C.; Eyre, D.R.
Eur. J. Biochem. 224, 943-950, 1994
A;Title: Structural characteristics of cross-linking sites in type V collagen of bone. C
A;Reference number: S48210; MUID:95010086; PMID:7925418
A;Accession: S65865
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <NIY>
A;Cross-references: UNIPARC:UPI000017C4E5

  Query Match             35.3%;  Score 18;  DB 2;  Length 9;
  Best Local Similarity   60.0%;  Pred. No. 2.8e+05;
  Matches    3;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 AGVGS 7
              :|:||
Db          4 SGLGS 8


RESULT 6
A41225
copper resistance protein A - Pseudomonas syringae pv. tomato (fragment)
C;Species: Pseudomonas syringae pv. tomato
C;Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 24-Jun-1993
C;Accession: A41225
R;Cha, J.S.; Cooksey, D.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 8915-8919, 1991
A;Title: Copper resistance in Pseudomonas syringae mediated by periplasmic and outer me
A;Reference number: A41225; MUID:92020961; PMID:1924351
A;Accession: A41225
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-5 <CHA>
A;Cross-references: UNIPARC:UPI000017A9B5

  Query Match             33.3%;  Score 17;  DB 2;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+05;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GSP 8
              |||
Db          3 GSP 5


RESULT 7
A27696
contraction-inhibiting peptide I - blue mussel
C;Species: Mytilus edulis (blue mussel)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C;Accession: A27696
R;Hirata, T.; Kubota, I.; Iwasawa, N.; Takabatake, I.; Ikeda, T.; Muneoka, Y.
Biochem. Biophys. Res. Commun. 152, 1376-1382, 1988
A;Title: Structures and actions of Mytilus inhibitory peptides.
A;Reference number: A90142; MUID:88240357; PMID:3377776
A;Accession: A27696
A;Molecule type: protein
A;Residues: 1-6 <HIR>
A;Cross-references: UNIPROT:P13736; UNIPARC:UPI00001279E1
C;Keywords: amidated carboxyl end
F;6/Modified site: amidated carboxyl end (Val) #status experimental

  Query Match             33.3%;  Score 17;  DB 2;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+05;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GSP 8
              |||
Db          1 GSP 3


RESULT 8
PT0627
T-cell receptor beta chain V-D-J region (100-2H) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0627
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0627
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-8 <FEE>
A;Cross-references: UNIPARC:UPI000017C7B1
```

A;Experimental source: newborn thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 33.3%; Score 17; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          3 AGVG 6
              ||:|
Db          5 AGLG 8
```

RESULT 9
PT0324
Ig heavy chain CRD3 region (clone J2-106C) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0324
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0324
A;Molecule type: DNA
A;Residues: 1-9 <YAM>
A;Cross-references: UNIPARC:UPI000017C217
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match 33.3%; Score 17; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          4 GVGSPY 9
              | | |
Db          3 GYGESY 8
```

RESULT 10
C39111
Ig heavy chain C region - Pacific hagfish (fragment)
C;Species: Eptatretus stouti (Pacific hagfish)
C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 16-Aug-1996
C;Accession: C39111
R;Varner, J.; Neame, P.; Litman, G.W.
Proc. Natl. Acad. Sci. U.S.A. 88, 1746-1750, 1991
A;Title: A serum heterodimer from hagfish (Eptatretus stoutii) exhibits structural simil
A;Reference number: A39111; MUID:91156684; PMID:2000382
A;Accession: C39111
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <VAR>
A;Cross-references: UNIPARC:UPI000017BF2B
C;Keywords: heterotetramer; immunoglobulin

Query Match 33.3%; Score 17; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```
Qy          5 VGSPYV 10
              : || |
Db          4 ISSPLV 9
```

RESULT 11
G60787
sperm-activating peptide (Ser-3,5,7 speract) - sea urchin (Anthocidaris crassispina)
C;Species: Anthocidaris crassispina
C;Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 16-Aug-2004
C;Accession: G60787
R;Suzuki, N.; Kajiura, H.; Nomura, K.; Garbers, D.L.; Yoshino, K.; Kurita, M.; Tanaka, H
Comp. Biochem. Physiol. B 89, 687-693, 1988
A;Title: Some more speract derivatives associated with eggs of sea urchins, Pseudocentro
A;Reference number: A60787; MUID:88242184; PMID:3378407
A;Accession: G60787
A;Molecule type: protein
A;Residues: 1-10 <SUZ>
A;Cross-references: UNIPROT:Q7M4D8; UNIPARC:UPI000017A4D6
C;Comment: This oligopeptide from egg jelly is one of several from this species, all o
at shows some, but not absolute, species restriction.

Query Match 33.3%; Score 17; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          3 AGVG 6
              :|||
Db          7 SGVG 10
```

RESULT 12
I60588
sperm-activating peptide (Glu-3,Met-4, Gly-5, Thr-7 SAP-I) - slate-pencil urchin (Hete
C;Species: Heterocentrotus mamillatus
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-2004
C;Accession: I60588
R;Yoshino, K.I.; Kajiura, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamag
Comp. Biochem. Physiol. B 94, 739-751, 1989
A;Title: A halogenated amino acid-containing sperm activating peptide and its related p
otus nudus, Echinometra mathaei and Heterocentrotus mammillatus.
A;Reference number: A60527
A;Accession: I60588
A;Molecule type: protein
A;Residues: 1-10 <YOS>
A;Cross-references: UNIPROT:Q7M4C0; UNIPARC:UPI000017A4EB

Query Match 33.3%; Score 17; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          2 MAGVG 6
              | | |
Db          4 MGGTG 8
```

RESULT 13
C23751
spinal cord peptide SCP-6 - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 28-Sep-1987 #sequence_revision 28-Sep-1987 #text_change 16-Aug-2004
C;Accession: C23751
R;Hsi, K.L.; Chen, R.L.; Chen, Z.G.; Zhang, H.L.; Lu, Y.A.; Guo, S.Y.; Wu, S.X.; Tsou,
Arch. Biochem. Biophys. 240, 178-183, 1985
A;Reference number: A23751; MUID:85250425; PMID:4015098
A;Accession: C23751
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-5 <HSI>
A;Cross-references: UNIPARC:UPI000017A4FA

Query Match 31.4%; Score 16; DB 2; Length 5;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          3 AGVG 6
              || |
Db          2 AGAG 5
```

RESULT 14
PT0623
T-cell receptor beta chain V-D-J region (111-1AB) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0623
R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0623
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-7 <FEE>
A;Cross-references: UNIPARC:UPI000017C7CB
A;Experimental source: newborn thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 31.4%; Score 16; DB 2; Length 7;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          3 AGVG 6
              || |
Db          4 AGTG 7
```

RESULT 15
PT0631
T-cell receptor beta chain V-D-J region (111-1I) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0631
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0631
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-8 <FEE>
A;Cross-references: UNIPARC:UPI000017C7D4
A;Experimental source: newborn thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 31.4%; Score 16; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          3 AGVG 6
              || |
Db          5 AGTG 8
```

Search completed: April 11, 2006, 19:23:18
Job time : 39 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 11, 2006, 19:15:49 ; Search time 229 Seconds
(without alignments)
30.809 Million cell updates/sec

Title: US-09-277-064-12
Perfect score: 51
Sequence: 1 VMAGVGSPYV 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 3063

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query % Match	Length	DB	ID	Description
1	24	47.1	8	2	Q8GTG5_LYCES	Q8gtg5 lycopersico
2	20	39.2	8	1	ALL16_CARMA	P81819 carcinus ma
3	20	39.2	8	1	ALL9_CARMA	P81812 carcinus ma
4	19	37.3	8	1	ALL5_CALVO	P41841 calliphora
5	19	37.3	9	2	Q6LDB5_HUMAN	Q6ldb5 homo sapien
6	19	37.3	9	2	Q9UQW0_HUMAN	Q9uqw0 homo sapien
7	19	37.3	10	2	Q67B09_9CAUD	Q67b09 bacteriopha
8	19	37.3	10	2	Q76MK9_9TELE	Q76mk9 eurypharynx
9	19	37.3	10	2	Q76MM5_9TELE	Q76mm5 eurypharynx
10	18	35.3	7	2	Q07624_9RETR	Q07624 rous sarcom
11	18	35.3	8	1	ALL7_CARMA	P81809 carcinus ma
12	18	35.3	10	1	FAR6_PANRE	P82660 panagrellus
13	18	35.3	10	2	Q7SA62_NEUCR	Q7sa62 neurospora
14	18	35.3	10	2	Q60HP3_9LABR	Q60hp3 xyrichtys d
15	17	33.3	6	1	CIP1_MYTED	P13736 mytilus edu
16	17	33.3	7	1	FAR1_HELTI	P41871 helisoma tr
17	17	33.3	8	1	DYS1_LIMIN	P82079 limnodynast
18	17	33.3	8	2	Q5ZEY7_HUMAN	Q5zey7 homo sapien
19	17	33.3	8	2	Q9R7T2_ECOLI	Q9r7t2 escherichia
20	17	33.3	9	2	Q4YFU0_PLABE	Q4yfu0 plasmodium
21	17	33.3	9	2	Q811S2_MOUSE	Q811s2 mus musculu
22	17	33.3	10	1	RT02_BOVIN	P82923 bos taurus
23	17	33.3	10	1	TKU2_UREUN	P40752 urechis uni
24	17	33.3	10	2	Q7M4C0_HETMA	Q7m4c0 heterocentr
25	17	33.3	10	2	Q4X386_PLACH	Q4x386 plasmodium
26	17	33.3	10	2	Q7M4D8_ANTCR	Q7m4d8 anthocidari
27	17	33.3	10	2	Q60HP1_9LABR	Q60hp1 cheilio ine
28	17	33.3	10	2	Q9PRY8_TRISC	Q9pry8 triakis scy
29	16	31.4	7	2	Q9BRY4_HUMAN	Q9bry4 homo sapien
30	16	31.4	7	2	Q8KMS3_9ENTR	Q8kms3 klebsiella
31	16	31.4	8	1	CAD1_ENTFA	P13268 enterococcu
32	16	31.4	8	1	VGLG_HHV2B	P81780 human herpe
33	16	31.4	8	2	Q7M4C6_PSEMC	Q7m4c6 pseudobolet
34	16	31.4	8	2	Q9GMH3_LAGOB	Q9gmh3 lagenorhync
35	16	31.4	9	2	Q7RA82_PLAYO	Q7ra82 plasmodium
36	16	31.4	9	2	Q7JIS3_LAGOB	Q7jis3 lagenorhync
37	16	31.4	9	2	Q7JIS4_LAGOL	Q7jis4 lagenorhync
38	16	31.4	9	2	Q7JIS5_LAGOL	Q7jis5 lagenorhync
39	16	31.4	9	2	Q7JIS6_LAGOL	Q7jis6 lagenorhync
40	16	31.4	9	2	Q7JIS7_LAGOL	Q7jis7 lagenorhync
41	16	31.4	9	2	Q7JIS8_LAGOL	Q7jis8 lagenorhync
42	16	31.4	9	2	Q7JIS9_LAGAC	Q7jis9 lagenorhync
43	16	31.4	9	2	Q7JIT0_LAGAC	Q7jit0 lagenorhync
44	16	31.4	9	2	Q7JIT1_LAGAC	Q7jit1 lagenorhync
45	16	31.4	9	2	Q9GJV1_LAGAC	Q9gjv1 lagenorhync

ALIGNMENTS

RESULT 1
Q8GTG5_LYCES
ID Q8GTG5_LYCES PRELIMINARY; PRT; 8 AA.
AC Q8GTG5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE WRKY transcription factor IId-1 splice variant 2 (Fragment).
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
OX NCBI_TaxID=4081;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Young leaves;
RA Cagna G., Boes A., Ulker B., Zhou A., Wanke D., Somssich I.E.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY157059; AAN71729.1; -; mRNA.
FT NON_TER 1 1
SQ SEQUENCE 8 AA; 917 MW; 59177B4775B87330 CRC64;

Query Match 47.1%; Score 24; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GSPY 9
||||
Db 3 GSPY 6

RESULT 2
ALL16_CARMA
ID ALL16_CARMA STANDARD; PRT; 8 AA.
AC P81819;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Carcinustatin-16.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidea; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -!- FUNCTION: May act as a neurotransmitter or neuromodulator.

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CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the allatostatin family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
KW   Amidation; Direct protein sequencing; Multigene family; Neuropeptide.
FT   MOD_RES       8      8       Leucine amide.
SQ   SEQUENCE   8 AA;  813 MW;  7C286B45AB476878 CRC64;

  Query Match             39.2%;  Score 20;  DB 1;  Length 8;
  Best Local Similarity   75.0%;  Pred. No. 2.2e+06;
  Matches    3;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 GSPY 9
              | ||
Db          1 GGPY 4


RESULT 3
ALL9_CARMA
ID   ALL9_CARMA     STANDARD;      PRT;     8 AA.
AC   P81812;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Carcinustatin-9.
OS   Carcinus maenas (Common shore crab) (Green crab).
OC   Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC   Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC   Eubrachyura; Portunoidea; Portunidae; Carcinus.
OX   NCBI_TaxID=6759;
RN   [1]
RP   PROTEIN SEQUENCE.
RC   TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX   MEDLINE=98121193; PubMed=9461295;
RA   Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA   Thorpe A.;
RT   "Isolation and identification of multiple neuropeptides of the
RT   allatostatin superfamily in the shore crab Carcinus maenas.";
RL   Eur. J. Biochem. 250:727-734(1997).
CC   -!- FUNCTION: May act as a neurotransmitter or neuromodulator.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the allatostatin family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
KW   Amidation; Direct protein sequencing; Multigene family; Neuropeptide.
FT   MOD_RES       8      8       Leucine amide.
SQ   SEQUENCE   8 AA;  781 MW;  7C2879CDCB476878 CRC64;

  Query Match             39.2%;  Score 20;  DB 1;  Length 8;
  Best Local Similarity   75.0%;  Pred. No. 2.2e+06;
  Matches    3;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 GSPY 9
              | ||
Db          1 GGPY 4


RESULT 4
ALL5_CALVO
ID   ALL5_CALVO     STANDARD;      PRT;     8 AA.
AC   P41841;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Callatostatin-5 (Met-callatostatin-1) ([Hyp3]Met-callatostatin).
OS   Calliphora vomitoria (Blue blowfly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC   Calliphoridae; Calliphora.
OX   NCBI_TaxID=27454;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=93211980; PubMed=8460157;
RA   Duve H., Johnsen A.H., Scott A.G., Yu C.G., Yagi K.J., Tobe S.S.,
RA   Thorpe A.;
RT   "Callatostatins: neuropeptides from the blowfly Calliphora vomitoria
RT   with sequence homology to cockroach allatostatins.";
RL   Proc. Natl. Acad. Sci. U.S.A. 90:2456-2460(1993).
RN   [2]
RP   CHARACTERIZATION, AND HYDROXYLATION.
RC   TISSUE=Head;
RX   MEDLINE=94342269; PubMed=8063725;
RA   Duve H., Johnsen A.H., Scott A.G., East P., Thorpe A.;
RT   "[Hyp3]Met-callatostatin. Identification and biological properties of
RT   a novel neuropeptide from the blowfly Calliphora vomitoria.";
RL   J. Biol. Chem. 269:21059-21066(1994).
CC   -!- FUNCTION: May act as a neurotransmitter or neuromodulator and play
CC       a role in the integration of information within the brain. May be
CC       involved in the control of visceral muscles due to its ability to
CC       behave as potent inhibitors of peristalic movements. May also
CC       fulfill a neurohormonal role on muscles of the gut and heart.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Neurons within brain and abdominal ganglion.
CC   -!- SIMILARITY: Belongs to the allatostatin family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   PIR; E47393; E47393.
KW   Amidation; Direct protein sequencing; Hydroxylation; Neuropeptide.
FT   MOD_RES       3      3       Hydroxyproline (partial).
FT   MOD_RES       8      8       Methionine amide.
SQ   SEQUENCE   8 AA;  883 MW;  7D9879CABB477768 CRC64;

  Query Match             37.3%;  Score 19;  DB 1;  Length 8;
  Best Local Similarity   75.0%;  Pred. No. 2.2e+06;
  Matches    3;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 GSPY 9
              | ||
Db          1 GPPY 4


RESULT 5
Q6LDB5_HUMAN
ID   Q6LDB5_HUMAN PRELIMINARY;      PRT;     9 AA.
AC   Q6LDB5;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Lamp-2 protein (Fragment).
GN   Name=lamp-2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=93286154; PubMed=8509432;
RA   Sawada R., Jardine K.A., Fukuda M.;
RT   "The genes of major lysosomal membrane glycoproteins lamp-1 and lamp-
RT   2. The 5'-flanking sequence of lamp-2 gene and comparison of exon
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RT   organization in two genes.";
RL   J. Biol. Chem. 268:13010-13010(1993).
DR   EMBL; S62577; AAB27101.1; -; Genomic_DNA.
FT   NON_TER       9      9
SQ   SEQUENCE   9 AA;  995 MW;  8C8EA5B877376DDA CRC64;

  Query Match           37.3%;  Score 19;  DB 2;  Length 9;
  Best Local Similarity   57.1%;  Pred. No. 2.2e+06;
  Matches    4;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 AGVGSPY 9
              | :|| |
Db          3 APLGSSY 9


RESULT 6
Q9UQW0_HUMAN
ID   Q9UQW0_HUMAN PRELIMINARY;      PRT;     9 AA.
AC   Q9UQW0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Prolactin precursor (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=84182507; PubMed=6325171;
RA   Truong A.T., Duez C., Belayew A., Renard A., Pictet R.L., Bell G.I.,
RA   Martial J.A.;
RT   "Isolation and characterization of the human prolactin gene.";
RL   EMBO J. 3:429-437(1984).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=93076813; PubMed=1332868;
RA   Peers B., Nalda A.M., Monget P., Voz M.L., Belayew A., Martial J.A.;
RT   "Binding of a 100-kDa ubiquitous factor to the human prolactin
RT   promoter is required for its basal and hormone-regulated activity.";
RL   Eur. J. Biochem. 210:53-58(1992).
DR   EMBL; X00368; CAA25108.1; -; Genomic_DNA.
KW   Signal.
FT   SIGNAL        <1      8       Potential.
FT   NON_TER        1      1
SQ   SEQUENCE   9 AA;  1060 MW;  0A1A6775B8733054 CRC64;

  Query Match           37.3%;  Score 19;  DB 2;  Length 9;
  Best Local Similarity   75.0%;  Pred. No. 2.2e+06;
  Matches    3;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GSPY 9
              |||:
Db          5 GSPW 8


RESULT 7
Q67B09_9CAUD
ID   Q67B09_9CAUD PRELIMINARY;      PRT;     10 AA.
AC   Q67B09;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   M4 protein (Fragment).
OS   Bacteriophage bIL170.
OC   Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX   NCBI_TaxID=63118;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Sousa A., Ze-Ze L., Parreira R., Tenreiro R., Silva P.;
RT   "Experimental phylogenies: picking a (the right) model.";
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY375289; AAR26461.1; -; Genomic_DNA.
FT   NON_TER       1      1
SQ   SEQUENCE   10 AA;  997 MW;  D38BBCC44732C87D CRC64;

  Query Match           37.3%;  Score 19;  DB 2;  Length 10;
  Best Local Similarity   80.0%;  Pred. No. 1.7e+04;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGV 5
              |:|||
Db          1 VVAGV 5


RESULT 8
Q76MK9_9TELE
ID   Q76MK9_9TELE PRELIMINARY;      PRT;     10 AA.
AC   Q76MK9;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   NADH dehydrogenase subunit 2 (Fragment).
GN   Name=ND2;
OS   Eurypharynx pelecanoides (pelican eel).
OG   Mitochondrion.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Anguilliformes;
OC   Eurypharyngidae; Eurypharynx.
OX   NCBI_TaxID=55117;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22967687; PubMed=12949142; DOI=10.1093/molbev/msg206;
RA   Inoue J.G., Miya M., Tsukamoto K., Nishida M.;
RT   "Evolution of the deep-sea gulper eel mitochondrial genomes: large-
RT   scale gene rearrangements originated within the eels.";
RL   Mol. Biol. Evol. 20:1917-1924(2003).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Inoue J., Inoue J., Miya M., Tsukamoto K., Nishida M.;
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB046485; BAB87156.1; -; Genomic_DNA.
DR   EMBL; AB046489; BAB87164.1; -; Genomic_DNA.
DR   EMBL; AB046481; BAB87148.1; -; Genomic_DNA.
DR   GO; GO:0005739; C:mitochondrion; IEA.
KW   Mitochondrion.
FT   NON_TER      10     10
SQ   SEQUENCE   10 AA;  1293 MW;  356FAE29C682DB47 CRC64;

  Query Match           37.3%;  Score 19;  DB 2;  Length 10;
  Best Local Similarity   75.0%;  Pred. No. 1.7e+04;
  Matches    3;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 SPYV 10
              :|||
Db          2 NPYV 5


RESULT 9
Q76MM5_9TELE
ID   Q76MM5_9TELE PRELIMINARY;      PRT;     10 AA.
AC   Q76MM5;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   NADH dehydrogenase subunit 2 (Fragment).
GN   Name=ND2;
OS   Eurypharynx pelecanoides (pelican eel).
OG   Mitochondrion.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Anguilliformes;
OC   Eurypharyngidae; Eurypharynx.
OX   NCBI_TaxID=55117;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
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RX   MEDLINE=22967687; PubMed=12949142; DOI=10.1093/molbev/msg206;
RA   Inoue J.G., Miya M., Tsukamoto K., Nishida M.;
RT   "Evolution of the deep-sea gulper eel mitochondrial genomes: large-
RT   scale gene rearrangements originated within the eels.";
RL   Mol. Biol. Evol. 20:1917-1924(2003).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Inoue J., Inoue J., Miya M., Tsukamoto K., Nishida M.;
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB046477; BAB87140.1; -; Genomic_DNA.
DR   GO; GO:0005739; C:mitochondrion; IEA.
KW   Mitochondrion.
FT   NON_TER      10     10
SQ   SEQUENCE   10 AA;  1261 MW;  357BFE29C682DB47 CRC64;

  Query Match           37.3%;  Score 19;  DB 2;  Length 10;
  Best Local Similarity   75.0%;  Pred. No. 1.7e+04;
  Matches    3;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 SPYV 10
              :|||
Db          2 NPYV 5


RESULT 10
Q07624_9RETR
ID   Q07624_9RETR PRELIMINARY;      PRT;     7 AA.
AC   Q07624;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   UORF1.
OS   Rous sarcoma virus.
OC   Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.
OX   NCBI_TaxID=11886;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Prague C;
RX   MEDLINE=93010967; PubMed=1327749;
RA   Donze O., Spahr P.F.;
RT   "Role of the open reading frames of Rous sarcoma virus leader RNA in
RT   translation and genome packaging.";
RL   EMBO J. 11:3747-3757(1992).
DR   EMBL; X67587; CAA47862.1; -; Genomic_RNA.
SQ   SEQUENCE   7 AA;  672 MW;  776045A7687DD6F0 CRC64;

  Query Match           35.3%;  Score 18;  DB 2;  Length 7;
  Best Local Similarity   57.1%;  Pred. No. 2.2e+06;
  Matches    4;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 MAGVGSP 8
              |||   |
Db          1 MAGPSIP 7


RESULT 11
ALL7_CARMA
ID   ALL7_CARMA     STANDARD;      PRT;     8 AA.
AC   P81809; P81804; P81810;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Carcinustatin-7 [Contains: Carcinustatin-6; Carcinustatin-1].
OS   Carcinus maenas (Common shore crab) (Green crab).
OC   Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC   Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC   Eubrachyura; Portunoidea; Portunidae; Carcinus.
OX   NCBI_TaxID=6759;
RN   [1]
RP   PROTEIN SEQUENCE.
RC   TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX   MEDLINE=98121193; PubMed=9461295;
RA   Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA   Thorpe A.;
RT   "Isolation and identification of multiple neuropeptides of the
RT   allatostatin superfamily in the shore crab Carcinus maenas.";
RL   Eur. J. Biochem. 250:727-734(1997).
CC   -!- FUNCTION: May act as a neurotransmitter or neuromodulator.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the allatostatin family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
KW   Amidation; Direct protein sequencing; Multigene family; Neuropeptide.
FT   PEPTIDE       1      8       Carcinustatin-7.
FT   PEPTIDE       2      8       Carcinustatin-6.
FT   PEPTIDE       4      8       Carcinustatin-1.
FT   MOD_RES       8      8       Leucine amide.
SQ   SEQUENCE   8 AA;  825 MW;  922879CDCB4775BD CRC64;

  Query Match           35.3%;  Score 18;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+06;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 SPY 9
              |||
Db          2 SPY 4


RESULT 12
FAR6_PANRE
ID   FAR6_PANRE     STANDARD;      PRT;     10 AA.
AC   P82660;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   FMRFamide-like neuropeptide PF6 (NGAPQPFVRF-amide).
OS   Panagrellus redivivus.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
OC   Panagrolaimoidea; Panagrolaimidae; Panagrellus.
OX   NCBI_TaxID=6233;
RN   [1]
RP   PROTEIN SEQUENCE, FUNCTION, AND AMIDATION.
RA   Moffett C.L., Marks N.J., Halton D.W., Thomson D.P., Geary T.G.,
RA   Maule A.G.;
RT   "Isolation, characterization and pharmacology of RMRFamide-related
RT   peptides (FaRPs) from free-living nematode, Panagrellus redivivus.";
RL   Submitted (JUL-2000) to Swiss-Prot.
CC   -!- FUNCTION: Myoactive.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC       family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
KW   Amidation; Direct protein sequencing; Neuropeptide.
FT   MOD_RES      10     10       Phenylalanine amide.
SQ   SEQUENCE   10 AA;  1132 MW;  CB13E4C9D776C76D CRC64;

  Query Match           35.3%;  Score 18;  DB 1;  Length 10;
  Best Local Similarity   42.9%;  Pred. No. 2.7e+04;
  Matches    3;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 GVGSPYV 10
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Db          2 GAPQPFV 8
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RESULT 13
Q7SA62_NEUCR
ID   Q7SA62_NEUCR PRELIMINARY;      PRT;    10 AA.
AC   Q7SA62;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Predicted protein.
GN   Name=NCU08327.1;
OS   Neurospora crassa.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX   NCBI_TaxID=5141;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=OR74A;
RA   Galagan J.E.,-Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA   Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA   Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA   Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA   Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA   Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA   Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA   Kamal M., Kamvysselis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
RA   Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,
RA   Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A.,
RA   DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA   Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA   Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA   Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;
RT   "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL   Nature 0:0-0(2003).
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AABX01000206; EAA33304.1; -; Genomic_DNA.
SQ   SEQUENCE   10 AA;  1284 MW;  D6D34CB72DC40059 CRC64;

  Query Match             35.3%;  Score 18;  DB 2;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+04;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 SPY 9
              |||
Db          8 SPY 10


RESULT 14
Q60HP3_9LABR
ID   Q60HP3_9LABR PRELIMINARY;      PRT;    10 AA.
AC   Q60HP3;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   NADH dehydrogenase subunit 1 (Fragment).
GN   Name=ND1;
OS   Xyrichtys dea.
OG   Mitochondrion.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
OC   Labridae; Xyrichtys.
OX   NCBI_TaxID=242818;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Mabuchi K., Miya M., Satoh T.P., Westneat M.W., Nishida M.;
RT   "Gene Rearrangements and Evolution of tRNA Pseudogenes in the
RT   Mitochondrial Genome of the Parrotfishes (Teleostei: Perciformes:
RT   Scaridae).";
RL   J. Mol. Evol. 59:287-297(2004).
DR   EMBL; AB117556; BAD51879.1; -; Genomic_DNA.
DR   GO; GO:0005739; C:mitochondrion; IEA.
KW   Mitochondrion.
FT   NON_TER       1      1
SQ   SEQUENCE   10 AA;  1030 MW;  4703C37760587DD7 CRC64;

  Query Match             35.3%;  Score 18;  DB 2;  Length 10;
  Best Local Similarity   37.5%;  Pred. No. 2.7e+04;
  Matches    3;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 MAGVGSPY 9
              :||:   |
Db          3 LAGIPPQY 10


RESULT 15
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ID   CIP1_MYTED     STANDARD;      PRT;     6 AA.
AC   P13736;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   01-FEB-2005 (Rel. 46, Last annotation update)
DE   Contraction-inhibiting peptide I (MIP I).
OS   Mytilus edulis (Blue mussel).
OC   Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
OC   Mytiloidea; Mytilidae; Mytilinae; Mytilus.
OX   NCBI_TaxID=6550;
RN   [1]
RP   PROTEIN SEQUENCE.
RC   TISSUE=Pedal ganglion;
RX   MEDLINE=88240357; PubMed=3377776;
RA   Hirata T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y.;
RT   "Structures and actions of Mytilus inhibitory peptides.";
RL   Biochem. Biophys. Res. Commun. 152:1376-1382(1988).
CC   -!- FUNCTION: Inhibitory action on contractions in several molluscan
CC       muscles.
CC   -!- SIMILARITY: To M.edulis MIP II.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   PIR; A27696; A27696.
KW   Amidation; Direct protein sequencing; Hormone.
FT   MOD_RES       6      6       Valine amide.
SQ   SEQUENCE   6 AA;  637 MW;  72C9C68775B81000 CRC64;

  Query Match             33.3%;  Score 17;  DB 1;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+06;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GSP 8
              |||
Db          1 GSP 3


Search completed: April 11, 2006, 19:22:35
Job time : 231 secs
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OM protein - protein search, using sw model

Run on: April 11, 2006, 19:34:56 ; Search time 47 Seconds
(without alignments)
17.591 Million cell updates/sec

Title: US-09-277-064-12
Perfect score: 51
Sequence: 1 VMAGVGSPYV 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
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4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	51	100.0	10	1	US-08-467-083-29	Sequence 29, Appl
2	51	100.0	10	1	US-08-414-417B-29	Sequence 29, Appl
3	51	100.0	10	1	US-08-486-348A-29	Sequence 29, Appl
4	51	100.0	10	1	US-08-468-545B-29	Sequence 29, Appl
5	51	100.0	10	2	US-08-466-680B-29	Sequence 29, Appl
6	51	100.0	10	2	US-09-341-982-95	Sequence 95, Appl
7	51	100.0	10	2	US-09-543-608A-16	Sequence 16, Appl
8	51	100.0	10	2	US-09-354-533-29	Sequence 29, Appl
9	51	100.0	10	4	PCT-US95-16415-12	Sequence 12, Appl
10	51	100.0	82	2	US-09-979-338A-27	Sequence 27, Appl
11	51	100.0	92	2	US-09-979-338A-31	Sequence 31, Appl
12	51	100.0	265	1	US-07-857-224B-66	Sequence 66, Appl
13	51	100.0	580	1	US-08-414-417B-69	Sequence 69, Appl
14	51	100.0	580	1	US-08-486-348A-69	Sequence 69, Appl
15	51	100.0	580	1	US-08-468-545B-69	Sequence 69, Appl
16	51	100.0	580	2	US-08-466-680B-69	Sequence 69, Appl
17	51	100.0	580	2	US-09-354-533-69	Sequence 69, Appl
18	51	100.0	1255	1	US-08-467-083-68	Sequence 68, Appl
19	51	100.0	1255	1	US-08-414-417B-68	Sequence 68, Appl
20	51	100.0	1255	1	US-08-484-438-8	Sequence 8, Appli
21	51	100.0	1255	1	US-08-486-348A-68	Sequence 68, Appl
22	51	100.0	1255	1	US-08-625-101-2	Sequence 2, Appli
23	51	100.0	1255	1	US-08-468-545B-68	Sequence 68, Appl
24	51	100.0	1255	1	US-08-356-786-2	Sequence 2, Appli
25	51	100.0	1255	2	US-08-466-680B-68	Sequence 68, Appl
26	51	100.0	1255	2	US-09-527-487-2	Sequence 2, Appli
27	51	100.0	1255	2	US-09-811-115-3	Sequence 3, Appli
28	51	100.0	1255	2	US-09-354-533-68	Sequence 68, Appl
29	51	100.0	1255	2	US-09-441-411-6	Sequence 6, Appli
30	51	100.0	1255	2	US-09-167-516-2	Sequence 2, Appli
31	47	92.2	9	2	US-09-527-487-9	Sequence 9, Appli
32	47	92.2	10	2	US-08-159-339A-263	Sequence 263, App
33	38	74.5	15	1	US-08-467-083-44	Sequence 44, Appl
34	38	74.5	15	1	US-08-414-417B-44	Sequence 44, Appl
35	38	74.5	15	1	US-08-486-348A-44	Sequence 44, Appl
36	38	74.5	15	1	US-08-468-545B-44	Sequence 44, Appl
37	38	74.5	15	2	US-08-466-680B-44	Sequence 44, Appl
38	38	74.5	15	2	US-09-354-533-44	Sequence 44, Appl
39	37	72.5	132	2	US-09-328-352-5435	Sequence 5435, Ap
40	37	72.5	210	2	US-09-107-433-4914	Sequence 4914, Ap
41	37	72.5	245	2	US-09-030-978A-2	Sequence 2, Appli
42	37	72.5	245	2	US-09-583-110-5152	Sequence 5152, Ap
43	36	70.6	44	2	US-10-318-675-81	Sequence 81, Appl
44	36	70.6	44	2	US-10-318-675-83	Sequence 83, Appl
45	36	70.6	643	2	US-09-949-016-10903	Sequence 10903, A

ALIGNMENTS

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RESULT 1
US-08-467-083-29
; Sequence 29, Application US/08467083
; Patent No. 5726023
;  GENERAL INFORMATION:
;    APPLICANT:  Cheever, Martin A.
;    APPLICANT:  Disis, Mary L.
;    TITLE OF INVENTION:  IMMUNE REACTIVITY TO HER-2/NEU PROTEIN
;    TITLE OF INVENTION:  FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
;    TITLE OF INVENTION:  HER-2/NEU ONCOGENE IS ASSOCIATED
;    NUMBER OF SEQUENCES:  68
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed and Berry
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  US
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/467,083
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/414,417
;      FILING DATE:  06-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sharkey, Richard G.
;      REGISTRATION NUMBER:  32,629
;      REFERENCE/DOCKET NUMBER:  920010.448C2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;      TELEX:  3723836 SEEDANBERRY
;  INFORMATION FOR SEQ ID NO:  29:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
US-08-467-083-29

  Query Match           100.0%;  Score 51;  DB 1;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0.0097;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 VMAGVGSPYV 10
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Db          1 VMAGVGSPYV 10


RESULT 2
US-08-414-417B-29
; Sequence 29, Application US/08414417B
; Patent No. 5801005
;  GENERAL INFORMATION:
;    APPLICANT:  Cheever, Martin A.
;    APPLICANT:  Disis, Mary L.
;    TITLE OF INVENTION:  IMMUNE REACTIVITY TO HER-2/neu PROTEIN
;    TITLE OF INVENTION:  FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
;    TITLE OF INVENTION:  HER-2/neu ONCOGENE IS ASSOCIATED
;    NUMBER OF SEQUENCES:  69
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed and Berry LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  US
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/414,417B
;      FILING DATE:  31-MAR-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sharkey, Richard G.
;      REGISTRATION NUMBER:  32,629
;      REFERENCE/DOCKET NUMBER:  920010.448C2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  29:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
US-08-414-417B-29

  Query Match             100.0%;  Score 51;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.0097;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db          1 VMAGVGSPYV 10


RESULT 3
US-08-486-348A-29
; Sequence 29, Application US/08486348A
; Patent No. 5846538
;  GENERAL INFORMATION:
;    APPLICANT:  Cheever, Martin A.
;    APPLICANT:  Disis, Mary L.
;    TITLE OF INVENTION:  IMMUNE REACTIVITY TO HER-2/neu PROTEIN
;    TITLE OF INVENTION:  FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
;    TITLE OF INVENTION:  HER-2/neu ONCOGENE IS ASSOCIATED
;    NUMBER OF SEQUENCES:  69
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed and Berry LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  US
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/486,348A
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sharkey, Richard G.
;      REGISTRATION NUMBER:  32,629
;      REFERENCE/DOCKET NUMBER:  920010.448C6
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  29:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
US-08-486-348A-29

  Query Match             100.0%;  Score 51;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.0097;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db          1 VMAGVGSPYV 10


RESULT 4
US-08-468-545B-29
; Sequence 29, Application US/08468545B
; Patent No. 5876712
;  GENERAL INFORMATION:
;    APPLICANT:  Cheever, Martin A.
;    APPLICANT:  Disis, Mary L.
;    TITLE OF INVENTION:  IMMUNE REACTIVITY TO HER-2/neu PROTEIN
;    TITLE OF INVENTION:  FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
;    TITLE OF INVENTION:  HER-2/neu ONCOGENE IS ASSOCIATED
;    NUMBER OF SEQUENCES:  69
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed and Berry LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  US
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/468,545B
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sharkey, Richard G.
;      REGISTRATION NUMBER:  32,629
;      REFERENCE/DOCKET NUMBER:  920010.448C5
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  29:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
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;      TOPOLOGY: linear
US-08-468-545B-29

  Query Match           100.0%;  Score 51;  DB 1;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0.0097;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
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Db          1 VMAGVGSPYV 10


RESULT 5
US-08-466-680B-29
; Sequence 29, Application US/08466680B
; Patent No. 6075122
;  GENERAL INFORMATION:
;    APPLICANT:  Cheever, Martin A.
;    APPLICANT:  Disis, Mary L.
;    TITLE OF INVENTION:  IMMUNE REACTIVITY TO HER-2/neu PROTEIN
;    TITLE OF INVENTION:  FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
;    TITLE OF INVENTION:  HER-2/neu ONCOGENE IS ASSOCIATED
;    NUMBER OF SEQUENCES:  69
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed and Berry LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  US
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/466,680B
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sharkey, Richard G.
;      REGISTRATION NUMBER:  32,629
;      REFERENCE/DOCKET NUMBER:  920010.448C4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  29:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
US-08-466-680B-29

  Query Match           100.0%;  Score 51;  DB 2;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0.0097;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db          1 VMAGVGSPYV 10


RESULT 6
US-09-341-982-95
; Sequence 95, Application US/09341982
; Patent No. 6558671
; GENERAL INFORMATION:
;  APPLICANT: SLINGLUFF, Craig L.
;  APPLICANT: HUNT, Donald F.
;  APPLICANT: ENGELHARD, Victor H.
;  APPLICANT: KITTLESEN, David
;  TITLE OF INVENTION: CYSTEINE-DEPLETED PEPTIDES RECOGNIZED BY A3-RESTRICTED
;  TITLE OF INVENTION: CYTOTOXIC LYMPHOCYTES, AND USES THEREFOR
;  FILE REFERENCE: SLINGLUFF=3B
;  CURRENT APPLICATION NUMBER: US/09/341,982
;  CURRENT FILING DATE: 1999-09-20
;  EARLIER APPLICATION NUMBER: PCT/US98/01592
;  EARLIER FILING DATE: 1998-01-29
;  EARLIER APPLICATION NUMBER: 60/037,781
;  EARLIER FILING DATE: 1997-01-31
;  NUMBER OF SEQ ID NOS: 104
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 95
;  LENGTH: 10
;  TYPE: PRT
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: Description of Artificial Sequence: Fragment of
;  OTHER INFORMATION: human protein
US-09-341-982-95

  Query Match           100.0%;  Score 51;  DB 2;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0.0097;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db          1 VMAGVGSPYV 10


RESULT 7
US-09-543-608A-16
; Sequence 16, Application US/09543608A
; Patent No. 6602510
; GENERAL INFORMATION:
;  APPLICANT: Fikes, John D.
;  APPLICANT:  Sette, Alessandro
;  APPLICANT:  Sidney, John
;  APPLICANT:  Southwood, Scott
;  APPLICANT:  Celis, Esteban
;  APPLICANT:  Keogh, Elissa A.
;  APPLICANT:  Chesnut, Robert
;  APPLICANT:  Epimmune Inc.
;  TITLE OF INVENTION: HLA Class I A2 Tumor Associated Antigen
;  TITLE OF INVENTION:  Peptides and Vaccine Compositions
;  FILE REFERENCE: 018623-015710US
;  CURRENT APPLICATION NUMBER: US/09/543,608A
;  CURRENT FILING DATE:  2002-04-05
;  NUMBER OF SEQ ID NOS: 52
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 16
;  LENGTH: 10
;  TYPE: PRT
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: Her2/neu.773
US-09-543-608A-16

  Query Match           100.0%;  Score 51;  DB 2;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0.0097;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db          1 VMAGVGSPYV 10


RESULT 8
US-09-354-533-29
; Sequence 29, Application US/09354533
; Patent No. 6664370
;  GENERAL INFORMATION:
;       APPLICANT: Cheever, Martin A.
;                  Disis, Mary L.
;       TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
```

```
;                          FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
;                          HER-2/neu ONCOGENE IS ASSOCIATED
;       NUMBER OF SEQUENCES: 69
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Seed and Berry LLP
;            STREET: 6300 Columbia Center, 701 Fifth Avenue
;            CITY: Seattle
;            STATE: Washington
;            COUNTRY: US
;            ZIP: 98104-7092
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/354,533
;            FILING DATE: 15-Jul-1999
;            CLASSIFICATION: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Sharkey, Richard G.
;            REGISTRATION NUMBER: 32,629
;            REFERENCE/DOCKET NUMBER: 920010.448C9
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (206) 622-4900
;            TELEFAX: (206) 682-6031
;   INFORMATION FOR SEQ ID NO: 29:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 10 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-09-354-533-29

  Query Match             100.0%;  Score 51;  DB 2;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.0097;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db          1 VMAGVGSPYV 10


RESULT 9
PCT-US95-16415-12
; Sequence 12, Application PC/TUS9516415
;  GENERAL INFORMATION:
;    APPLICANT:  The Scripps Research Institute
;    TITLE OF INVENTION:  IN VIVO ACTIVATION OF TUMOR-SPECIFIC
;    TITLE OF INVENTION:  CYTOTOXIC T CELLS
;    NUMBER OF SEQUENCES:  38
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  The Scripps Research Institute
;      STREET:  10666 North Torrey Pines Road, TPC-8
;      CITY:  La Jolla
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/16415
;      FILING DATE:  13-DEC-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/355,558
;      FILING DATE:  14-DEC-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Logan, April C.
;      REGISTRATION NUMBER:  33,950
;      REFERENCE/DOCKET NUMBER:  433.1PC
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 554-2937
;      TELEFAX:  (619) 554-6312
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
PCT-US95-16415-12

  Query Match             100.0%;  Score 51;  DB 4;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.0097;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db          1 VMAGVGSPYV 10


RESULT 10
US-09-979-338A-27
; Sequence 27, Application US/09979338A
; Patent No. 6846622
; GENERAL INFORMATION:
;  APPLICANT: Heffron et al.
;  TITLE OF INVENTION: Tagged Epitope Protein Transposable Element
;  FILE REFERENCE: 61589
;  CURRENT APPLICATION NUMBER: US/09/979,338A
;  CURRENT FILING DATE:  2001-11-21
;  PRIOR APPLICATION NUMBER: PCT/US00/14687
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: 60/136,210
;  PRIOR FILING DATE: 1999-05-26
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
;   LENGTH: 82
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Amino acid
;   OTHER INFORMATION: resolved product using the construct shown in FIG
;   OTHER INFORMATION: 5.
US-09-979-338A-27

  Query Match             100.0%;  Score 51;  DB 2;  Length 82;
  Best Local Similarity   100.0%;  Pred. No. 0.077;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db         40 VMAGVGSPYV 49


RESULT 11
US-09-979-338A-31
; Sequence 31, Application US/09979338A
; Patent No. 6846622
; GENERAL INFORMATION:
;  APPLICANT: Heffron et al.
;  TITLE OF INVENTION: Tagged Epitope Protein Transposable Element
;  FILE REFERENCE: 61589
;  CURRENT APPLICATION NUMBER: US/09/979,338A
;  CURRENT FILING DATE:  2001-11-21
;  PRIOR APPLICATION NUMBER: PCT/US00/14687
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: 60/136,210
;  PRIOR FILING DATE: 1999-05-26
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 31
;   LENGTH: 92
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Amino acid
;   OTHER INFORMATION: resolved product using the construct shown in f
;   OTHER INFORMATION: FIG 9.
US-09-979-338A-31

  Query Match            100.0%;  Score 51;  DB 2;  Length 92;
  Best Local Similarity  100.0%;  Pred. No. 0.086;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db         47 VMAGVGSPYV 56


RESULT 12
US-07-857-224B-66
; Sequence 66, Application US/07857224B
; Patent No. 5958784
;  GENERAL INFORMATION:
;    APPLICANT:  Benner, Steven A.
;    TITLE OF INVENTION:  Predicting Folded Structures of Proteins
;    NUMBER OF SEQUENCES:  114
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Steven A. Benner
;      STREET:  Hadlaubstrasse 151
;      CITY:  Zurich
;      STATE:  none
;      COUNTRY:  Switzerland
;      ZIP:  (note: this is an international post code) CH-8092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch diskette, 1.4 Mb storage
;      COMPUTER:  Apple MacIntosh
;      OPERATING SYSTEM:  MacIntosh 7.0
;      SOFTWARE:  Microsoft Word
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/857,224B
;      FILING DATE:  03/25/92
;      CLASSIFICATION:  436
;    PRIOR APPLICATION DATA:  none
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (International) 41 1 632 2830
;      TELEFAX:  (International) 41 1 262 2437
;      TELEX:  none
;  INFORMATION FOR SEQ ID NO:  66:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  265
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:
;      DESCRIPTION:  protein
;    ORIGINAL SOURCE:
;      ORGANISM:  human
;    FEATURE:  Protein kinase; Table 8 Column 75
;    PUBLICATION INFORMATION:
;      AUTHORS:
;      AUTHORS:  Hanks, S. K.
;      AUTHORS:  Quinn, A. M.
;      AUTHORS:  Hunter, T.
;      TITLE:  The protein kinase family
;      JOURNAL:  Science
;      VOLUME:  241
;      PAGES:  42-52
;      DATE:  1988
US-07-857-224B-66

  Query Match            100.0%;  Score 51;  DB 1;  Length 265;
  Best Local Similarity  100.0%;  Pred. No. 0.24;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db         56 VMAGVGSPYV 65


RESULT 13
US-08-414-417B-69
; Sequence 69, Application US/08414417B
; Patent No. 5801005
;  GENERAL INFORMATION:
;    APPLICANT:  Cheever, Martin A.
;    APPLICANT:  Disis, Mary L.
;    TITLE OF INVENTION:  IMMUNE REACTIVITY TO HER-2/neu PROTEIN
;    TITLE OF INVENTION:  FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
;    TITLE OF INVENTION:  HER-2/neu ONCOGENE IS ASSOCIATED
;    NUMBER OF SEQUENCES:  69
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed and Berry LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  US
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/414,417B
;      FILING DATE:  31-MAR-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sharkey, Richard G.
;      REGISTRATION NUMBER:  32,629
;      REFERENCE/DOCKET NUMBER:  920010.448C2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  69:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  580 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
US-08-414-417B-69

  Query Match            100.0%;  Score 51;  DB 1;  Length 580;
  Best Local Similarity  100.0%;  Pred. No. 0.52;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db         98 VMAGVGSPYV 107


RESULT 14
US-08-486-348A-69
; Sequence 69, Application US/08486348A
; Patent No. 5846538
;  GENERAL INFORMATION:
;    APPLICANT:  Cheever, Martin A.
;    APPLICANT:  Disis, Mary L.
;    TITLE OF INVENTION:  IMMUNE REACTIVITY TO HER-2/neu PROTEIN
;    TITLE OF INVENTION:  FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
;    TITLE OF INVENTION:  HER-2/neu ONCOGENE IS ASSOCIATED
;    NUMBER OF SEQUENCES:  69
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed and Berry LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
```

```
;       COUNTRY:  US
;       ZIP:  98104-7092
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/486,348A
;       FILING DATE:  07-JUN-1995
;       CLASSIFICATION:  424
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Sharkey, Richard G.
;       REGISTRATION NUMBER:  32,629
;       REFERENCE/DOCKET NUMBER:  920010.448C6
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (206) 622-4900
;       TELEFAX:  (206) 682-6031
;   INFORMATION FOR SEQ ID NO:  69:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  580 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:
;       TOPOLOGY:  linear
US-08-486-348A-69

  Query Match             100.0%;  Score 51;  DB 1;  Length 580;
  Best Local Similarity   100.0%;  Pred. No. 0.52;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db         98 VMAGVGSPYV 107


RESULT 15
US-08-468-545B-69
; Sequence 69, Application US/08468545B
; Patent No. 5876712
;  GENERAL INFORMATION:
;    APPLICANT:  Cheever, Martin A.
;    APPLICANT:  Disis, Mary L.
;    TITLE OF INVENTION:  IMMUNE REACTIVITY TO HER-2/neu PROTEIN
;    TITLE OF INVENTION:  FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
;    TITLE OF INVENTION:  HER-2/neu ONCOGENE IS ASSOCIATED
;    NUMBER OF SEQUENCES:  69
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed and Berry LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  US
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/468,545B
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sharkey, Richard G.
;      REGISTRATION NUMBER:  32,629
;      REFERENCE/DOCKET NUMBER:  920010.448C5
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  69:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  580 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
US-08-468-545B-69

  Query Match             100.0%;  Score 51;  DB 1;  Length 580;
  Best Local Similarity   100.0%;  Pred. No. 0.52;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db         98 VMAGVGSPYV 107


Search completed:  April 11, 2006, 19:36:15
Job time :  47 secs
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OM protein - protein search, using sw model

Run on: April 11, 2006, 19:35:40 ; Search time 166 Seconds
(without alignments)
25.170 Million cell updates/sec

Title: US-09-277-064-12
Perfect score: 51
Sequence: 1 VMAGVGSPYV 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	51	100.0	10	2	US-08-812-393A-49	Sequence 49, Appl
2	51	100.0	10	3	US-09-354-533-29	Sequence 29, Appl
3	51	100.0	10	3	US-09-277-074-12	Sequence 12, Appl
4	51	100.0	10	3	US-09-277-064-12	Sequence 12, Appl
5	51	100.0	10	3	US-09-774-681-49	Sequence 49, Appl
6	51	100.0	10	4	US-10-080-013-16	Sequence 16, Appl
7	51	100.0	10	4	US-10-245-871-620	Sequence 620, App
8	51	100.0	10	4	US-10-149-138-786	Sequence 786, App
9	51	100.0	10	4	US-10-149-138-2352	Sequence 2352, Ap
10	51	100.0	10	4	US-10-149-138-4335	Sequence 4335, Ap
11	51	100.0	10	4	US-10-149-138-4422	Sequence 4422, Ap
12	51	100.0	10	4	US-10-149-138-4435	Sequence 4435, Ap
13	51	100.0	10	4	US-10-253-286-620	Sequence 620, App
14	51	100.0	10	4	US-10-289-566-16	Sequence 16, Appl
15	51	100.0	10	4	US-10-333-430-31	Sequence 31, Appl
16	51	100.0	10	4	US-10-647-005-29	Sequence 29, Appl
17	51	100.0	10	4	US-10-149-138-786	Sequence 786, App
18	51	100.0	10	4	US-10-149-138-2352	Sequence 2352, Ap
19	51	100.0	10	4	US-10-149-138-4335	Sequence 4335, Ap
20	51	100.0	10	4	US-10-149-138-4422	Sequence 4422, Ap
21	51	100.0	10	4	US-10-149-138-4435	Sequence 4435, Ap
22	51	100.0	10	6	US-11-121-347-29	Sequence 29, Appl
23	51	100.0	11	4	US-10-149-138-838	Sequence 838, App
24	51	100.0	11	4	US-10-149-138-2386	Sequence 2386, Ap
25	51	100.0	11	4	US-10-149-138-838	Sequence 838, App
26	51	100.0	11	4	US-10-149-138-2386	Sequence 2386, Ap
27	51	100.0	15	4	US-10-149-138-3728	Sequence 3728, Ap
28	51	100.0	15	4	US-10-149-138-3736	Sequence 3736, Ap
29	51	100.0	15	4	US-10-149-138-4473	Sequence 4473, Ap
30	51	100.0	15	4	US-10-149-138-4500	Sequence 4500, Ap
31	51	100.0	15	4	US-10-149-138-4562	Sequence 4562, Ap
32	51	100.0	15	4	US-10-149-138-3728	Sequence 3728, Ap
33	51	100.0	15	4	US-10-149-138-3736	Sequence 3736, Ap
34	51	100.0	15	4	US-10-149-138-4473	Sequence 4473, Ap
35	51	100.0	15	4	US-10-149-138-4500	Sequence 4500, Ap
36	51	100.0	15	4	US-10-149-138-4562	Sequence 4562, Ap
37	51	100.0	18	3	US-09-734-520-24	Sequence 24, Appl
38	51	100.0	18	4	US-10-012-034A-24	Sequence 24, Appl
39	51	100.0	23	4	US-10-245-871-622	Sequence 622, App
40	51	100.0	23	4	US-10-253-286-622	Sequence 622, App
41	51	100.0	126	4	US-10-333-430-70	Sequence 70, Appl
42	51	100.0	171	5	US-10-482-029-247	Sequence 247, App
43	51	100.0	289	5	US-10-801-266-6	Sequence 6, Appli
44	51	100.0	391	5	US-10-949-667-6	Sequence 6, Appli
45	51	100.0	570	4	US-10-378-393-15	Sequence 15, Appl

ALIGNMENTS

```
RESULT 1
US-08-812-393A-49
; Sequence 49, Application US/08812393A
; Publication No. US20010007152A1
;  GENERAL INFORMATION:
;    APPLICANT:  SHERMAN, Linda A.
;    APPLICANT:  LUSTGARTEN, Joseph
;    TITLE OF INVENTION:  RECOMBINANT CONSTRUCTS ENCODING
;    TITLE OF INVENTION:  T CELL RECEPTORS SPECIFIC FOR HUMAN HLA-RESTRICTED TUMOR
;    TITLE OF INVENTION:  ANTIGENS
;    NUMBER OF SEQUENCES:  64
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  2000 Pennsylvania Avenue, NW, suite 5500
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20006-1888
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/812,393A
;      FILING DATE:  05-MAR-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  31333-20001.00
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-887-1500
;      TELEFAX:  202-822-0168
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  49:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-812-393A-49

  Query Match           100.0%;  Score 51;  DB 2;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0.016;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 VMAGVGSPYV 10
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Db          1 VMAGVGSPYV 10


RESULT 2
US-09-354-533-29
; Sequence 29, Application US/09354533
; Publication No. US20020055614A1
;  GENERAL INFORMATION:
;       APPLICANT: Cheever, Martin A.
;                  Disis, Mary L.
;       TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
;                           FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
;                           HER-2/neu ONCOGENE IS ASSOCIATED
;       NUMBER OF SEQUENCES: 69
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Seed and Berry LLP
;            STREET: 6300 Columbia Center, 701 Fifth Avenue
;            CITY: Seattle
;            STATE: Washington
;            COUNTRY: US
;            ZIP: 98104-7092
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/354,533
;            FILING DATE: 15-Jul-1999
;            CLASSIFICATION: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Sharkey, Richard G.
;            REGISTRATION NUMBER: 32,629
;            REFERENCE/DOCKET NUMBER: 920010.448C9
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (206) 622-4900
;            TELEFAX: (206) 682-6031
;   INFORMATION FOR SEQ ID NO: 29:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 10 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-09-354-533-29

  Query Match             100.0%;  Score 51;  DB 3;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.016;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db          1 VMAGVGSPYV 10


RESULT 3
US-09-277-074-12
; Sequence 12, Application US/09277074
; Publication No. US20030022820A1
; GENERAL INFORMATION:
;  APPLICANT:  Sherman, Linda A.
;  TITLE OF INVENTION:  IN VIVO ACTIVATION OF TUMOR-SPECIFIC CYTOTOXIC T CELLS
;  FILE REFERENCE:  SCR2155S
;  CURRENT APPLICATION NUMBER: US/09/277,074
;  CURRENT FILING DATE:  1999-03-26
;  PRIOR APPLICATION NUMBER:  08/355,558
;  PRIOR FILING DATE:  1994-12-14
;  PRIOR APPLICATION NUMBER:  PCT/US95/16415
;  PRIOR FILING DATE:  1995-12-14
;  NUMBER OF SEQ ID NOS:  39
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 12
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-277-074-12

  Query Match             100.0%;  Score 51;  DB 3;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.016;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db          1 VMAGVGSPYV 10


RESULT 4
US-09-277-064-12
; Sequence 12, Application US/09277064
; Publication No. US20030064916A1
; GENERAL INFORMATION:
;  APPLICANT:  Sherman, Linda A.
;  TITLE OF INVENTION:  IN VIVO ACTIVATION OF TUMOR-SPECIFIC CYTOTOXIC T CELLS
;  FILE REFERENCE:  SCR2152S
;  CURRENT APPLICATION NUMBER: US/09/277,064
;  CURRENT FILING DATE:  1999-03-26
;  PRIOR APPLICATION NUMBER:  08/355,558
;  PRIOR FILING DATE:  1994-12-14
;  PRIOR APPLICATION NUMBER:  PCT/US95/16415
;  PRIOR FILING DATE:  1995-12-14
;  NUMBER OF SEQ ID NOS:  39
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 12
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-277-064-12

  Query Match             100.0%;  Score 51;  DB 3;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.016;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db          1 VMAGVGSPYV 10


RESULT 5
US-09-774-681-49
; Sequence 49, Application US/09774681
; Publication No. US20030208780A1
; GENERAL INFORMATION:
;  APPLICANT: Sunol Molecular Corporatiopn
;  APPLICANT:  Sherman, Linda
;  APPLICANT:  Lustgarten, Joseph
;  TITLE OF INVENTION: RECOMBINANT CONSTRUCTS ENCODING T CELL
;  TITLE OF INVENTION:  RECEPTORS SPECIFIC FOR HUMAN HLA-RESTRICTED TUMOR ANTIGENS
;  FILE REFERENCE: 31333-20001.01
;  CURRENT APPLICATION NUMBER: US/09/774,681
;  CURRENT FILING DATE:  2001-02-01
;  PRIOR APPLICATION NUMBER: US 08/812,393
;  PRIOR FILING DATE: 1997-03-05
;  PRIOR APPLICATION NUMBER: US 60/012,845
;  PRIOR FILING DATE: 1996-03-05
;  NUMBER OF SEQ ID NOS: 65
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 49
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthesized peptide
US-09-774-681-49
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  Query Match           100.0%;  Score 51;  DB 3;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0.016;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db          1 VMAGVGSPYV 10


RESULT 6
US-10-080-013-16
; Sequence 16, Application US/10080013
; Publication No. US20030077248A1
; GENERAL INFORMATION:
;  APPLICANT: Moriarty, Ann
;  APPLICANT:  Leturcq, Didier
;  APPLICANT:  Degraw, Juli
;  APPLICANT:  Heiskala, Marja
;  APPLICANT:  Peterson, Per
;  APPLICANT:  Jackson, Michael
;  TITLE OF INVENTION: A CELL THERAPY METHOD FOR THE TREATMENT OF TUMORS
;  FILE REFERENCE: ORT-1557
;  CURRENT APPLICATION NUMBER: US/10/080,013
;  CURRENT FILING DATE:  2002-02-19
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-080-013-16

  Query Match           100.0%;  Score 51;  DB 4;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0.016;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db          1 VMAGVGSPYV 10


RESULT 7
US-10-245-871-620
; Sequence 620, Application US/10245871
; Publication No. US20030235594A1
; GENERAL INFORMATION:
;  APPLICANT: HUMPHREYS, ROBERT
;  APPLICANT:  XU, MINZHEN
;  TITLE OF INVENTION: Ii-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
;  FILE REFERENCE: REH-2013
;  CURRENT APPLICATION NUMBER: US/10/245,871
;  CURRENT FILING DATE:  2003-01-09
;  PRIOR APPLICATION NUMBER: 10/197,000
;  PRIOR FILING DATE: 2002-07-17
;  PRIOR APPLICATION NUMBER: 09/396,813
;  PRIOR FILING DATE: 1999-09-14
;  NUMBER OF SEQ ID NOS: 905
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 620
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-245-871-620

  Query Match           100.0%;  Score 51;  DB 4;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0.016;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db          1 VMAGVGSPYV 10


RESULT 8
US-10-149-138-786
; Sequence 786, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
;  APPLICANT: Fikes, John
;  APPLICANT:  Sette, Alessandro
;  APPLICANT:  Sidney, John
;  APPLICANT:  Southwood, Scott
;  APPLICANT:  Chesnut, Robert
;  APPLICANT:  Celis, Esteban
;  APPLICANT:  Keogh, Elissa
;  TITLE OF INVENTION: Inducing Cellular Immune Responses to
;  TITLE OF INVENTION:  HER2/neu Using Peptide and Nucleic Acid Compositions
;  FILE REFERENCE: 2060.0140001
;  CURRENT APPLICATION NUMBER: US/10/149,138
;  CURRENT FILING DATE:  2002-06-10
;  PRIOR APPLICATION NUMBER: PCT/US00/33591
;  PRIOR FILING DATE: 2000-12-11
;  PRIOR APPLICATION NUMBER: US 09/458,299
;  PRIOR FILING DATE: 1999-12-11
;  NUMBER OF SEQ ID NOS: 4641
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 786
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-786

  Query Match           100.0%;  Score 51;  DB 4;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0.016;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db          1 VMAGVGSPYV 10


RESULT 9
US-10-149-138-2352
; Sequence 2352, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
;  APPLICANT: Fikes, John
;  APPLICANT:  Sette, Alessandro
;  APPLICANT:  Sidney, John
;  APPLICANT:  Southwood, Scott
;  APPLICANT:  Chesnut, Robert
;  APPLICANT:  Celis, Esteban
;  APPLICANT:  Keogh, Elissa
;  TITLE OF INVENTION: Inducing Cellular Immune Responses to
;  TITLE OF INVENTION:  HER2/neu Using Peptide and Nucleic Acid Compositions
;  FILE REFERENCE: 2060.0140001
;  CURRENT APPLICATION NUMBER: US/10/149,138
;  CURRENT FILING DATE:  2002-06-10
;  PRIOR APPLICATION NUMBER: PCT/US00/33591
;  PRIOR FILING DATE: 2000-12-11
;  PRIOR APPLICATION NUMBER: US 09/458,299
;  PRIOR FILING DATE: 1999-12-11
;  NUMBER OF SEQ ID NOS: 4641
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2352
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-2352

  Query Match           100.0%;  Score 51;  DB 4;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0.016;
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  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db          1 VMAGVGSPYV 10


RESULT 10
US-10-149-138-4335
; Sequence 4335, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
;  APPLICANT: Fikes, John
;  APPLICANT:  Sette, Alessandro
;  APPLICANT:  Sidney, John
;  APPLICANT:  Southwood, Scott
;  APPLICANT:  Chesnut, Robert
;  APPLICANT:  Celis, Esteban
;  APPLICANT:  Keogh, Elissa
;  TITLE OF INVENTION: Inducing Cellular Immune Responses to
;  TITLE OF INVENTION:  HER2/neu Using Peptide and Nucleic Acid Compositions
;  FILE REFERENCE: 2060.0140001
;  CURRENT APPLICATION NUMBER: US/10/149,138
;  CURRENT FILING DATE:  2002-06-10
;  PRIOR APPLICATION NUMBER: PCT/US00/33591
;  PRIOR FILING DATE: 2000-12-11
;  PRIOR APPLICATION NUMBER: US 09/458,299
;  PRIOR FILING DATE: 1999-12-11
;  NUMBER OF SEQ ID NOS: 4641
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4335
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Artificial Peptide
US-10-149-138-4335

  Query Match             100.0%;  Score 51;  DB 4;  Length 10;
  Best Local Similarity   100.0%;  Pred. No: 0.016;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db          1 VMAGVGSPYV 10


RESULT 11
US-10-149-138-4422
; Sequence 4422, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
;  APPLICANT: Fikes, John
;  APPLICANT:  Sette, Alessandro
;  APPLICANT:  Sidney, John
;  APPLICANT:  Southwood, Scott
;  APPLICANT:  Chesnut, Robert
;  APPLICANT:  Celis, Esteban
;  APPLICANT:  Keogh, Elissa
;  TITLE OF INVENTION: Inducing Cellular Immune Responses to
;  TITLE OF INVENTION:  HER2/neu Using Peptide and Nucleic Acid Compositions
;  FILE REFERENCE: 2060.0140001
;  CURRENT APPLICATION NUMBER: US/10/149,138
;  CURRENT FILING DATE:  2002-06-10
;  PRIOR APPLICATION NUMBER: PCT/US00/33591
;  PRIOR FILING DATE: 2000-12-11
;  PRIOR APPLICATION NUMBER: US 09/458,299
;  PRIOR FILING DATE: 1999-12-11
;  NUMBER OF SEQ ID NOS: 4641
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4422
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Artificial Peptide
US-10-149-138-4422

  Query Match             100.0%;  Score 51;  DB 4;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.016;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db          1 VMAGVGSPYV 10


RESULT 12
US-10-149-138-4435
; Sequence 4435, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
;  APPLICANT: Fikes, John
;  APPLICANT:  Sette, Alessandro
;  APPLICANT:  Sidney, John
;  APPLICANT:  Southwood, Scott
;  APPLICANT:  Chesnut, Robert
;  APPLICANT:  Celis, Esteban
;  APPLICANT:  Keogh, Elissa
;  TITLE OF INVENTION: Inducing Cellular Immune Responses to
;  TITLE OF INVENTION:  HER2/neu Using Peptide and Nucleic Acid Compositions
;  FILE REFERENCE: 2060.0140001
;  CURRENT APPLICATION NUMBER: US/10/149,138
;  CURRENT FILING DATE:  2002-06-10
;  PRIOR APPLICATION NUMBER: PCT/US00/33591
;  PRIOR FILING DATE: 2000-12-11
;  PRIOR APPLICATION NUMBER: US 09/458,299
;  PRIOR FILING DATE: 1999-12-11
;  NUMBER OF SEQ ID NOS: 4641
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4435
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Artificial Peptide
US-10-149-138-4435

  Query Match             100.0%;  Score 51;  DB 4;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.016;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db          1 VMAGVGSPYV 10


RESULT 13
US-10-253-286-620
; Sequence 620, Application US/10253286
; Publication No. US20040058881A1
; GENERAL INFORMATION:
;  APPLICANT: HUMPHREYS, ROBERT
;  APPLICANT:  XU, MINZHEN
;  TITLE OF INVENTION: Ii-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
;  FILE REFERENCE: REH-2015
;  CURRENT APPLICATION NUMBER: US/10/253,286
;  CURRENT FILING DATE:  2003-01-13
;  PRIOR APPLICATION NUMBER: 10/197,000
;  PRIOR FILING DATE: 2002-07-17
;  PRIOR APPLICATION NUMBER: 09/396,813
;  PRIOR FILING DATE: 1999-09-14
;  NUMBER OF SEQ ID NOS: 905
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 620
;   LENGTH: 10
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;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-253-286-620

  Query Match           100.0%;  Score 51;  DB 4;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0.016;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db          1 VMAGVGSPYV 10


RESULT 14
US-10-289-566-16
; Sequence 16, Application US/10289566
; Publication No. US20040071671A1
; GENERAL INFORMATION:
;  APPLICANT: Leturcq, Didier J.
;  APPLICANT:  Moriarty, Ann M.
;  APPLICANT:  Jackson, Michael R.
;  APPLICANT:  Peterson, Per A.
;  APPLICANT:  Richards, Jon M.
;  TITLE OF INVENTION: A CELL THERAPY METHOD FOR THE TREATMENT OF TUMORS
;  FILE REFERENCE: ORT 1342CIP
;  CURRENT APPLICATION NUMBER: US/10/289,566
;  CURRENT FILING DATE:  2002-11-07
;  PRIOR APPLICATION NUMBER: US 60/270,252
;  PRIOR FILING DATE: 2001-02-20
;  PRIOR APPLICATION NUMBER: US 10/080,013
;  PRIOR FILING DATE: 2002-02-19
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-289-566-16

  Query Match           100.0%;  Score 51;  DB 4;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0.016;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db          1 VMAGVGSPYV 10


RESULT 15
US-10-333-430-31
; Sequence 31, Application US/10333430
; Publication No. US20040072240A1
; GENERAL INFORMATION:
;  APPLICANT: INSERM
;  APPLICANT:  INSTITUT GUSTAVE ROUSSY
;  APPLICANT:  KOSMATOPOULOS, Kostas
;  APPLICANT:  TOURDOT, Sophie
;  APPLICANT:  SCARDINO, Antonio
;  APPLICANT:  GROSS, David, Alexandre
;  TITLE OF INVENTION: METHOD FOR SCREENING PEPTIDES FOR USE IN
;  TITLE OF INVENTION:  IMMUNOTHERAPY
;  FILE REFERENCE: 33339/259034
;  CURRENT APPLICATION NUMBER: US/10/333,430
;  CURRENT FILING DATE:  2003-10-02
;  PRIOR APPLICATION NUMBER: FR 0009591
;  PRIOR FILING DATE: 2000-07-21
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic peptide
US-10-333-430-31

  Query Match           100.0%;  Score 51;  DB 4;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0.016;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db          1 VMAGVGSPYV 10


Search completed: April 11, 2006, 19:39:07
Job time : 167 secs
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OM protein - protein search, using sw model

Run on: April 11, 2006, 19:36:30 ; Search time 25 Seconds
(without alignments)
12.477 Million cell updates/sec

Title: US-09-277-064-12
Perfect score: 51
Sequence: 1 VMAGVGSPYV 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 184161 seqs, 31191982 residues

Total number of hits satisfying chosen parameters: 184161

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /SIDS5/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
2: /SIDS5/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /SIDS5/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /SIDS5/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
5: /SIDS5/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
6: /SIDS5/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /SIDS5/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /SIDS5/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	51	100.0	10	7	US-11-033-039-620	Sequence 620, App
2	51	100.0	23	7	US-11-033-039-622	Sequence 622, App
3	51	100.0	82	6	US-10-968-629-27	Sequence 27, Appl
4	51	100.0	92	6	US-10-968-629-31	Sequence 31, Appl
5	51	100.0	1255	6	US-10-770-726-62	Sequence 62, Appl
6	51	100.0	1255	7	US-11-022-562-213	Sequence 213, App
7	51	100.0	1255	7	US-11-113-202-10	Sequence 10, Appl
8	51	100.0	1255	7	US-11-033-039-553	Sequence 553, App
9	51	100.0	1255	7	US-11-155-288-9	Sequence 9, Appli
10	51	100.0	1255	7	US-11-202-516-4	Sequence 4, Appli
11	51	100.0	1255	7	US-11-175-405-2	Sequence 2, Appli
12	51	100.0	1258	7	US-11-033-039-930	Sequence 930, App
13	42	82.4	19	7	US-11-033-039-931	Sequence 931, App
14	41	80.4	9	6	US-10-510-101-135	Sequence 135, App
15	38	74.5	15	7	US-11-033-039-908	Sequence 908, App
16	38	74.5	20	7	US-11-033-039-932	Sequence 932, App
17	36	70.6	44	6	US-10-957-887B-209	Sequence 209, App
18	36	70.6	44	6	US-10-957-887B-251	Sequence 251, App
19	36	70.6	161	7	US-11-098-686-11415	Sequence 11415, A
20	35	68.6	19	7	US-11-033-039-933	Sequence 933, App
21	35	68.6	217	7	US-11-096-568A-16847	Sequence 16847, A
22	35	68.6	506	7	US-11-055-822-946	Sequence 946, App
23	35	68.6	730	7	US-11-082-389-358	Sequence 358, App
24	34	66.7	374	7	US-11-072-175-148	Sequence 148, App
25	34	66.7	435	7	US-11-087-099-3138	Sequence 3138, Ap
26	34	66.7	462	7	US-11-082-389-412	Sequence 412, App
27	34	66.7	1433	7	US-11-094-519A-40	Sequence 40, Appl
28	33	64.7	112	7	US-11-230-180-17	Sequence 17, Appl
29	33	64.7	358	7	US-11-087-099-11741	Sequence 11741, A
30	33	64.7	363	7	US-11-087-099-2715	Sequence 2715, Ap
31	33	64.7	363	7	US-11-087-099-3776	Sequence 3776, Ap
32	33	64.7	363	7	US-11-087-099-4337	Sequence 4337, Ap
33	33	64.7	491	7	US-11-098-686-10836	Sequence 10836, A
34	33	64.7	748	7	US-11-096-568A-34369	Sequence 34369, A
35	32	62.7	208	7	US-11-096-568A-22891	Sequence 22891, A
36	32	62.7	237	7	US-11-096-568A-33599	Sequence 33599, A
37	32	62.7	256	7	US-11-096-568A-22890	Sequence 22890, A
38	32	62.7	284	7	US-11-096-568A-33598	Sequence 33598, A
39	32	62.7	313	7	US-11-087-099-257	Sequence 257, App
40	32	62.7	313	7	US-11-096-568A-33597	Sequence 33597, A
41	32	62.7	324	7	US-11-087-099-10913	Sequence 10913, A
42	32	62.7	324	7	US-11-051-720-1349	Sequence 1349, Ap
43	32	62.7	344	7	US-11-087-099-7157	Sequence 7157, Ap
44	32	62.7	362	7	US-11-087-099-1068	Sequence 1068, Ap
45	32	62.7	369	7	US-11-087-099-9241	Sequence 9241, Ap

ALIGNMENTS

RESULT 1
US-11-033-039-620
; Sequence 620, Application US/11033039
; Publication No. US20060002947A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2017US01
; CURRENT APPLICATION NUMBER: US/11/033,039
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 10/245,871
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 620
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-033-039-620

Query Match 100.0%; Score 51; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00065;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VMAGVGSPYV 10
||||||||||
Db 1 VMAGVGSPYV 10

RESULT 2
US-11-033-039-622
; Sequence 622, Application US/11033039
; Publication No. US20060002947A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2017US01
; CURRENT APPLICATION NUMBER: US/11/033,039
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 10/245,871
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197,000

; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 622
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: hybrid peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (5)..(5)
; OTHER INFORMATION: Ava
US-11-033-039-622

Query Match 100.0%; Score 51; DB 7; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VMAGVGSPYV 10
||||||||||
Db 6 VMAGVGSPYV 15

RESULT 3
US-10-968-629-27
; Sequence 27, Application US/10968629
; Publication No. US20060040382A1
; GENERAL INFORMATION:
; APPLICANT: Heffron et al.
; TITLE OF INVENTION: Tagged Epitope Protein Transposable Element
; FILE REFERENCE: 61589
; CURRENT APPLICATION NUMBER: US/10/968,629
; CURRENT FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: 09/979,338
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: PCT/US00/14687
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/136,210
; PRIOR FILING DATE: 1999-05-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid
; OTHER INFORMATION: resolved product using the construct shown in FIG
; OTHER INFORMATION: 5.
US-10-968-629-27

Query Match 100.0%; Score 51; DB 6; Length 82;
Best Local Similarity 100.0%; Pred. No. 0.0063;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VMAGVGSPYV 10
||||||||||
Db 40 VMAGVGSPYV 49

RESULT 4
US-10-968-629-31
; Sequence 31, Application US/10968629
; Publication No. US20060040382A1
; GENERAL INFORMATION:
; APPLICANT: Heffron et al.
; TITLE OF INVENTION: Tagged Epitope Protein Transposable Element
; FILE REFERENCE: 61589
; CURRENT APPLICATION NUMBER: US/10/968,629
; CURRENT FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: 09/979,338
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: PCT/US00/14687
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/136,210
; PRIOR FILING DATE: 1999-05-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid
; OTHER INFORMATION: resolved product using the construct shown in f
; OTHER INFORMATION: FIG 9.
US-10-968-629-31

Query Match 100.0%; Score 51; DB 6; Length 92;
Best Local Similarity 100.0%; Pred. No. 0.0072;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VMAGVGSPYV 10
||||||||||
Db 47 VMAGVGSPYV 56

RESULT 5
US-10-770-726-62
; Sequence 62, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATI
; TITLE OF INVENTION: CANCERS
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 62
; LENGTH: 1255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-770-726-62

Query Match 100.0%; Score 51; DB 6; Length 1255;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VMAGVGSPYV 10
||||||||||
Db 773 VMAGVGSPYV 782

RESULT 6
US-11-022-562-213
; Sequence 213, Application US/11022562
; Publication No. US20050249742A1
; GENERAL INFORMATION:
; APPLICANT: Ruprecht, Ruth M.
; APPLICANT: Shisong, Jiang
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
; TITLE OF INVENTION: A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE
; FILE REFERENCE: DFN-043CN
; CURRENT APPLICATION NUMBER: US/11/022,562
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: PCT/US03/20322
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 60/392718

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;  PRIOR FILING DATE: 2002-06-27
;  NUMBER OF SEQ ID NOS: 340
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 213
;    LENGTH: 1255
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-11-022-562-213

  Query Match             100.0%;  Score 51;  DB 7;  Length 1255;
  Best Local Similarity   100.0%;  Pred. No. 0.12;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db        773 VMAGVGSPYV 782


RESULT 7
US-11-113-202-10
; Sequence 10, Application US/11113202
; Publication No. US20050272637A1
; GENERAL INFORMATION:
;  APPLICANT: Clinton, Gail M.
;  APPLICANT:  Shamieh, Lara
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR  MODULATING SIGNALING BY IGF-1
;  TITLE OF INVENTION:  RECEPTOR AND ERBB RECEPTORS
;  FILE REFERENCE: 49321-136
;  CURRENT APPLICATION NUMBER: US/11/113,202
;  CURRENT FILING DATE:  2005-04-22
;  PRIOR APPLICATION NUMBER: US 60/590,473
;  PRIOR FILING DATE: 2004-07-23
;  PRIOR APPLICATION NUMBER: US 60/564,893
;  PRIOR FILING DATE: 2004-04-22
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10
;    LENGTH: 1255
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-11-113-202-10

  Query Match             100.0%;  Score 51;  DB 7;  Length 1255;
  Best Local Similarity   100.0%;  Pred. No. 0.12;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db        773 VMAGVGSPYV 782


RESULT 8
US-11-033-039-553
; Sequence 553, Application US/11033039
; Publication No. US20060002947A1
; GENERAL INFORMATION:
;  APPLICANT: HUMPHREYS, ROBERT
;  APPLICANT:  XU, MINZHEN
;  TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
;  FILE REFERENCE: REH-2017US01
;  CURRENT APPLICATION NUMBER: US/11/033,039
;  CURRENT FILING DATE:  2005-01-11
;  PRIOR APPLICATION NUMBER: 10/245,871
;  PRIOR FILING DATE: 2002-09-17
;  PRIOR APPLICATION NUMBER: 10/197,000
;  PRIOR FILING DATE: 2002-07-17
;  PRIOR APPLICATION NUMBER: 09/396,813
;  PRIOR FILING DATE: 1999-09-14
;  NUMBER OF SEQ ID NOS: 1452
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 553
;    LENGTH: 1255
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-11-033-039-553

  Query Match             100.0%;  Score 51;  DB 7;  Length 1255;
  Best Local Similarity   100.0%;  Pred. No. 0.12;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db        773 VMAGVGSPYV 782


RESULT 9
US-11-155-288-9
; Sequence 9, Application US/11155288
; Publication No. US20060008468A1
; GENERAL INFORMATION:
;  APPLICANT: Chiang, Chih-Sheng
;  APPLICANT:  Simard, John J.L.
;  TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED
;  TITLE OF INVENTION:  ANTIGENS IN DIAGNOSTICS FOR VARIOUS TYPES OF CANCERS
;  FILE REFERENCE: MANNK.050A
;  CURRENT APPLICATION NUMBER: US/11/155,288
;  CURRENT FILING DATE:  2005-06-17
;  PRIOR APPLICATION NUMBER: 60/580,969
;  PRIOR FILING DATE: 2004-06-17
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;    LENGTH: 1255
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-11-155-288-9

  Query Match             100.0%;  Score 51;  DB 7;  Length 1255;
  Best Local Similarity   100.0%;  Pred. No. 0.12;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db        773 VMAGVGSPYV 782


RESULT 10
US-11-202-516-4
; Sequence 4, Application US/11202516
; Publication No. US20060008465A1
; GENERAL INFORMATION:
;  APPLICANT: Steinaa, Lucilla
;  APPLICANT:  Mouritsen, Soren
;  APPLICANT:  Gautam, Anand
;  APPLICANT:  Dalum, Iben
;  APPLICANT:  Haaning, Jesper
;  APPLICANT:  Leach, Dana
;  APPLICANT:  Nielsen, Klaus
;  APPLICANT:  Karlsson, Gunilla
;  APPLICANT:  Rasmussen, Peter
;  TITLE OF INVENTION: Novel Methods for Therapeutic Vaccination
;  FILE REFERENCE: 4614-0107PUS2
;  CURRENT APPLICATION NUMBER: US/11/202,516
;  CURRENT FILING DATE:  2005-08-11
;  PRIOR APPLICATION NUMBER: US 09/806,703
;  PRIOR FILING DATE: 2001-04-04
;  PRIOR APPLICATION NUMBER: PCT/DK99/00525
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: DK 1998 01261
;  PRIOR FILING DATE: 1998-10-05
;  PRIOR APPLICATION NUMBER: US 60/105,011
;  PRIOR FILING DATE: 1998-10-20
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
;    LENGTH: 1255
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-202-516-4

Query Match 100.0%; Score 51; DB 7; Length 1255;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VMAGVGSPYV 10
||||||||||
Db 773 VMAGVGSPYV 782

RESULT 11
US-11-175-405-2
; Sequence 2, Application US/11175405
; Publication No. US20060019344A1
; GENERAL INFORMATION:
; APPLICANT: STUART, SUSAN G.
; APPLICANT: MONAHAN, JOHN J.
; APPLICANT: LANGTON, BEATRICE CLAUDIA
; APPLICANT: HANCOCK, MIRIAM E.C.
; APPLICANT: CHAO, LORRINE A.
; APPLICANT: BLUFORD, PETER
; TITLE OF INVENTION: C-ERBB-2 EXTERNAL DOMAIN: GP75
; FILE REFERENCE: BEBIO-111-C1
; CURRENT APPLICATION NUMBER: US/11/175,405
; CURRENT FILING DATE: 2005-07-07
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-405-2

Query Match 100.0%; Score 51; DB 7; Length 1255;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VMAGVGSPYV 10
||||||||||
Db 773 VMAGVGSPYV 782

RESULT 12
US-11-033-039-930
; Sequence 930, Application US/11033039
; Publication No. US20060002947A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2017US01
; CURRENT APPLICATION NUMBER: US/11/033,039
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 10/245,871
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 930
; LENGTH: 1258
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-033-039-930

Query Match 100.0%; Score 51; DB 7; Length 1258;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VMAGVGSPYV 10
||||||||||
Db 773 VMAGVGSPYV 782

RESULT 13
US-11-033-039-931
; Sequence 931, Application US/11033039
; Publication No. US20060002947A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2017US01
; CURRENT APPLICATION NUMBER: US/11/033,039
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 10/245,871
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 931
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: hybrid peptide
US-11-033-039-931

Query Match 82.4%; Score 42; DB 7; Length 19;
Best Local Similarity 88.9%; Pred. No. 0.068;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 MAGVGSPYV 10
| |||||||
Db 3 MKGVGSPYV 11

RESULT 14
US-10-510-101-135
; Sequence 135, Application US/10510101
; Publication No. US20060018915A1
; GENERAL INFORMATION:
; APPLICANT: Epimmune Inc.
; APPLICANT: Ishioka, Glenn
; APPLICANT: Fikes, John
; APPLICANT: Tangri, Shabnam
; APPLICANT: Sette, Alessandro
; TITLE OF INVENTION: Heteroclitic Analogs and Related Methods
; FILE REFERENCE: 2060.009PC05
; CURRENT APPLICATION NUMBER: US/10/510,101
; CURRENT FILING DATE: 2004-10-05
; PRIOR APPLICATION NUMBER: US 60/413,471
; PRIOR FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 10/116,118
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 135
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide derived from Homo sapiens Her2/neu
US-10-510-101-135

Query Match 80.4%; Score 41; DB 6; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.4e+05;

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  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPY 9
              || ||||||
Db          1 VMDGVGSPY 9


RESULT 15
US-11-033-039-908
; Sequence 908, Application US/11033039
; Publication No. US20060002947A1
; GENERAL INFORMATION:
;  APPLICANT: HUMPHREYS, ROBERT
;  APPLICANT:  XU, MINZHEN
;  TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
;  FILE REFERENCE: REH-2017US01
;  CURRENT APPLICATION NUMBER: US/11/033,039
;  CURRENT FILING DATE:  2005-01-11
;  PRIOR APPLICATION NUMBER: 10/245,871
;  PRIOR FILING DATE: 2002-09-17
;  PRIOR APPLICATION NUMBER: 10/197,000
;  PRIOR FILING DATE: 2002-07-17
;  PRIOR APPLICATION NUMBER: 09/396,813
;  PRIOR FILING DATE: 1999-09-14
;  NUMBER OF SEQ ID NOS: 1452
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 908
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-033-039-908

  Query Match             74.5%;  Score 38;  DB 7;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 0.3;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 GVGSPYV 10
              |||||||
Db          1 GVGSPYV 7


Search completed: April 11, 2006, 19:39:38
Job time : 26 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 11, 2006, 19:31:00 ; Search time 38 Seconds
(without alignments)
25.320 Million cell updates/sec

Title: US-09-277-064-12
Perfect score: 51
Sequence: 1 VMAGVGSPYV 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	51	100.0	1255	1	A24571	protein-tyrosine k
2	51	100.0	1260	1	TVRTNU	protein-tyrosine k
3	48	94.1	1254	2	I48161	p-185 precursor -
4	39	76.5	348	2	T09037	hypothetical prote
5	38	74.5	381	2	A69091	cell division prot
6	38	74.5	697	1	S04987	SITS-binding prote
7	37	72.5	247	2	B95109	uridylate kinase [
8	37	72.5	247	2	E97977	UMP kinase (EC 2.7
9	37	72.5	288	2	F70780	hypothetical prote
10	37	72.5	388	2	G90450	hypothetical prote
11	37	72.5	1020	2	D83679	hypothetical prote
12	36	70.6	66	2	T35138	hypothetical prote
13	36	70.6	224	2	D46177	enhancer of split
14	36	70.6	275	1	WMBEH4	UL34 protein - hum
15	36	70.6	625	2	S65829	hypothetical prote
16	36	70.6	639	2	B48189	sodium/phosphate c
17	36	70.6	921	2	AC1327	isoleucyl-tRNA syn
18	36	70.6	921	2	AE1698	isoleucyl-tRNA syn
19	35	68.6	261	2	E83150	hypothetical prote
20	35	68.6	277	2	AD3358	2-dehydro-3-deoxy-
21	35	68.6	286	2	S76153	hypothetical prote
22	35	68.6	288	2	AI1966	permease protein o
23	35	68.6	435	2	AD2583	two component sens
24	35	68.6	481	2	B97365	helO protein U4905
25	35	68.6	529	1	H70736	IMP dehydrogenase
26	35	68.6	529	1	S72823	IMP dehydrogenase
27	35	68.6	598	2	S10893	transforming prote
28	35	68.6	616	1	RRVQLL	probable RNA-direc
29	35	68.6	616	1	RRVQWA	probable RNA-direc
30	35	68.6	698	2	I39713	celB protein - Agr
31	35	68.6	756	2	S74929	adenylate cyclase
32	35	68.6	827	2	AC2963	celB protein [impo
33	35	68.6	881	2	B98320	cellulose synthase
34	34	66.7	240	2	E89899	uridylate kinase [
35	34	66.7	276	2	E72623	probable autoantig
36	34	66.7	307	2	B95099	membrane protein [
37	34	66.7	307	2	A97967	conserved hypothet
38	34	66.7	391	2	A70663	probable PPE prote
39	34	66.7	434	2	AE1326	hypothetical prote
40	34	66.7	434	2	AG1697	hypothetical prote
41	34	66.7	610	2	S41315	hypothetical prote
42	34	66.7	662	2	C97507	hypothetical prote
43	34	66.7	662	2	AG2725	2',3'-cyclic-nucle
44	34	66.7	938	2	AH0058	isoleucine-tRNA li
45	34	66.7	1427	2	I51669	tumor suppressor -

ALIGNMENTS

RESULT 1
A24571
protein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - human
N;Alternate names: c-erb-B-2 protein precursor; kinase-related transforming protein er
C;Species: Homo sapiens (man)
C;Date: 25-Oct-1987 #sequence_revision 06-Dec-1996 #text_change 05-Oct-2004
C;Accession: A24571; A25491; A44188; B44188; I59509; I57622
R;Yamamoto, T.; Ikawa, S.; Akiyama, T.; Semba, K.; Nomura, N.; Miyajima, N.; Saito, T.
Nature 319, 230-234, 1986
A;Title: Similarity of protein encoded by the human c-erb-B-2 gene to epidermal growth
A;Reference number: A24571; MUID:86118663; PMID:3003577
A;Accession: A24571
A;Molecule type: mRNA
A;Residues: 1-1255 <YAM>
A;Cross-references: UNIPROT:P04626; UNIPARC:UPI000003F55F; GB:X03363; NID:g31197; PIDN
R;Semba, K.; Kamata, N.; Toyoshima, K.; Yamamoto, T.
Proc. Natl. Acad. Sci. U.S.A. 82, 6497-6501, 1985
A;Title: A v-erbB-related protooncogene, c-erbB-2, is distinct from the c-erbB-1/epide
A;Reference number: A25491; MUID:86016729; PMID:2995967
A;Accession: A25491
A;Molecule type: DNA
A;Residues: 737-1031 <SEM>
A;Cross-references: UNIPARC:UPI000016A8A7; GB:M11767; NID:g182163; PIDN:AAA35808.1; PI
R;Coussens, L.; Yang-Feng, T.L.; Liao, Y.C.; Chen, E.; Gray, A.; McGrath, J.; Seeburg,
Science 230, 1132-1139, 1985
A;Title: Tyrosine kinase receptor with extensive homology to EGF receptor shares chrom
A;Reference number: A44188; MUID:86070181; PMID:2999974
A;Accession: A44188
A;Molecule type: DNA
A;Residues: 740-910 <COU1>.
A;Cross-references: UNIPARC:UPI000016AA26; GB:M12036; NID:g183988; PIDN:AAA35978.1; PI
A;Accession: B44188
A;Molecule type: mRNA
A;Residues: 1-517,'RALL',522,'S',524-654,'V',656-1169,'A',1171-1255 <COU2>
A;Cross-references: UNIPARC:UPI00001725C7; GB:M11730; NID:g183986
R;King, C.R.; Kraus, M.H.; Aaronson, S.A.
Science 229, 974-976, 1985
A;Title: Amplification of a novel v-erbB-related gene in a human mammary carcinoma.
A;Reference number: I59509; MUID:85272597; PMID:2992089
A;Accession: I59509
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 832-909 <REX>
A;Cross-references: UNIPARC:UPI0000070A3F; GB:L29395; NID:g459807; PIDN:AAA35809.1; PI
R;Tal, M.; King, C.R.; Kraus, M.H.; Ullrich, A.; Schlessinger, J.; Givol, D.
Mol. Cell. Biol. 7, 2597-2601, 1987
A;Title: Human HER2 (neu) promoter: evidence for multiple mechanisms for transcription
A;Reference number: I57622; MUID:87286898; PMID:3039351
A;Accession: I57622
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-191 <TAL>

A;Cross-references: UNIPARC:UPI0000000427; GB:M16792; NID:g183983; PIDN:AAA58637.1; PID:
C;Comment: Amplification and overexpression of this erbB-related gene occurs in about 30
C;Genetics:
A;Gene: GDB:ERBB2; NGL; NEU; HER-2
A;Cross-references: GDB:120613; OMIM:164870
A;Map position: 17q21.1-17q21.1
A;Introns: 25/1; 75/3; 147/1; 883/3
A;Note: the list of introns is incomplete
C;Function:
A;Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
C;Superfamily: Tyrosine-protein kinase, EGF receptor type; protein kinase homology
C;Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphoprotein; phospho
inase
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-1255/Product: protein-tyrosine kinase erbB2 #status predicted <MAT>
F;22-653/Domain: extracellular #status predicted <EXT>
F;70-304/Domain: EGF receptor extracellular domain repeat <EE1>
F;395-605/Domain: EGF receptor extracellular domain repeat <EE2>
F;654-675/Domain: transmembrane #status predicted <TMM>
F;676-1255/Domain: intracellular #status predicted <INT>
F;718-983/Domain: protein kinase homology <KIN>
F;726-734/Region: protein kinase ATP-binding motif
F;68,124,187,259,530,571,629/Binding site: carbohydrate (Asn) (covalent) #status predict
F;686/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
F;753/Active site: Lys #status predicted
F;1139,1221,1222,1248/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation)

Query Match 100.0%; Score 51; DB 1; Length 1255;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VMAGVGSPYV 10
||||||||||
Db 773 VMAGVGSPYV 782

RESULT 2
TVRTNU
protein-tyrosine kinase (EC 2.7.1.112) neu precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 05-Oct-2004
C;Accession: A24562; A61204
R;Bargmann, C.I.; Hung, M.C.; Weinberg, R.A.
Nature 319, 226-230, 1986
A;Title: The neu oncogene encodes an epidermal growth factor receptor-related protein.
A;Reference number: A24562; MUID:86118662; PMID:3945311
A;Accession: A24562
A;Molecule type: mRNA
A;Residues: 1-1260 <BAR>
A;Cross-references: UNIPROT:P06494; UNIPARC:UPI0000161B83; EMBL:X03362; NID:g56745; PIDN
R;Masui, T.; Mann, A.M.; Macatee, T.L.; Garland, E.M.; Okamura, T.; Smith, R.A.; Cohen,
Carcinogenesis 12, 1975-1978, 1991
A;Title: Direct DNA sequencing of the rat neu oncogene transmembrane domain reveals no m
2-thiazolyl]formamide or N-methyl-N-nitrosourea.
A;Reference number: A61204; MUID:92035293; PMID:1682063
A;Accession: A61204
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 637-663,'V',665-702 <MAS>
A;Cross-references: UNIPARC:UPI00001725C8
A;Note: authors translated the codon GCA for residue 25 as Val
C;Genetics:
A;Gene: neu
C;Superfamily: Tyrosine-protein kinase, EGF receptor type; protein kinase homology
C;Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphoprotein; phospho
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-1260/Product: protein-tyrosine kinase neu #status predicted <MAT>
F;658-680/Domain: transmembrane #status predicted <TMN>
F;723-988/Domain: protein kinase homology <KIN>
F;731-739/Region: protein kinase ATP-binding motif
F;71,191,263,535,576,634/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;691/Binding site: phosphate (Thr) (covalent) #status predicted
F;758/Active site: Lys #status predicted
F;882,1227,1253/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 100.0%; Score 51; DB 1; Length 1260;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VMAGVGSPYV 10
||||||||||
Db 778 VMAGVGSPYV 787

RESULT 3
I48161
p-185 precursor - golden hamster
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Oct-2004
C;Accession: I48161
R;Nakamura, T.; Ushijima, T.; Ishizaka, Y.; Nagao, M.; Arai, M.; Yamazaki, Y.; Ishikaw
Gene 140, 251-255, 1994
A;Title: Cloning and activation of the Syrian hamster neu proto-oncogene.
A;Reference number: I48161; MUID:94193007; PMID:7908275
A;Accession: I48161
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1254 <RES>
A;Cross-references: UNIPROT:Q60553; UNIPARC:UPI000012A111; GB:D16295; NID:g493236; PID
C;Genetics:
A;Gene: neu
C;Superfamily: Tyrosine-protein kinase, EGF receptor type; protein kinase homology
C;Keywords: ATP
F;718-983/Domain: protein kinase homology <KIN>
F;726-734/Region: protein kinase ATP-binding motif

Query Match 94.1%; Score 48; DB 2; Length 1254;
Best Local Similarity 90.0%; Pred. No. 0.82;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VMAGVGSPYV 10
||||:|||||
Db 773 VMAGLGSPYV 782

RESULT 4
T09037
hypothetical protein F26K10.90 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T09037
R;Bevan, M.; Lennard, N.; Quail, M.; Harris, B.; Rajandream, M.A.; Barrell, B.G.; Banc
submitted to the Protein Sequence Database, June 1999
A;Reference number: Z16533
A;Accession: T09037
A;Molecule type: DNA
A;Residues: 1-348 <BEV>
A;Cross-references: UNIPROT:Q9M0I6; UNIPARC:UPI000009E5E1; EMBL:AL049803; GSPDB:GN0006
A;Experimental source: cultivar Columbia; BAC clone F26K10
C;Genetics:
A;Gene: ATSP:F26K10.90
A;Map position: 4
A;Introns: 120/1
C;Superfamily: Arabidopsis thaliana hypothetical protein F26K10.90

Query Match 76.5%; Score 39; DB 2; Length 348;
Best Local Similarity 70.0%; Pred. No. 12;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VMAGVGSPYV 10
|:|||| |:|
Db 276 VLAGVGEPWV 285

RESULT 5
A69091

cell division protein FtsZ - Methanobacterium thermoautotrophicum (strain Delta H)
C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: A69091
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Accession: A69091
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-381 <MTH>
A;Cross-references: UNIPROT:O27712; UNIPARC:UPI000012AD23; GB:AE000925; GB:AE000666; NID
A;Experimental source: strain Delta H
C;Genetics:
A;Gene: MTH1676
A;Start codon: TTG
C;Superfamily: cell division protein ftsZ
F;133-139/Region: tubulin/FtsZ GTP/GDP-binding (G-G-G-T-G-[ST]-G) motif

  Query Match 74.5%; Score 38; DB 2; Length 381;
  Best Local Similarity 70.0%; Pred. No. 20;
  Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VMAGVGSPYV 10
 |:||| |||:
Db 337 VVAGVRSPYI 346

RESULT 6
S04987
SITS-binding protein sp105 - Pacific electric ray
C;Species: Torpedo californica (Pacific electric ray)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C;Accession: S04987; S30070
R;Jentsch, T.J.; Garcia, A.M.; Lodish, H.F.
Biochem. J. 261, 155-166, 1989
A;Title: Primary structure of a novel 4-acetamido-4'-isothiocyanostilbene-2,2'-disulphon
A;Reference number: S04987; MUID:89374082; PMID:2775201
A;Accession: S04987
A;Molecule type: mRNA
A;Residues: 1-697 <JEN1>
A;Cross-references: UNIPROT:P19965; UNIPARC:UPI00001714BC; EMBL:X16078; NID:g64403; PIDN
A;Accession: S30070
A;Molecule type: protein
A;Residues: 2-11;435-449,'X',451-452,'X',454-459;634-649 <JEN2>
A;Cross-references: UNIPARC:UPI0000174107; UNIPARC:UPI0000174108; UNIPARC:UPI0000174109
C;Superfamily: SITS-binding protein sp105
C;Keywords: disulfide bond; glycoprotein; homodimer; transmembrane protein
F;2-697/Product: SITS-binding protein #status experimental <MAT>
F;30-50/Domain: transmembrane #status predicted <TM1>
F;503-521/Domain: transmembrane #status predicted <TM2>
F;542-562/Domain: transmembrane #status predicted <TM3>
F;25,112,134,162,386,405,470,568/Binding site: carbohydrate (Asn) (covalent) #status pre

  Query Match 74.5%; Score 38; DB 1; Length 697;
  Best Local Similarity 100.0%; Pred. No. 36;
  Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GVGSPYV 10
 |||||||
Db 436 GVGSPYV 442

RESULT 7
B95109
uridylate kinase [imported] - Streptococcus pneumoniae (strain TIGR4)
C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Accession: B95109
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrisc
A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: B95109
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-247 <KUR>
A;Cross-references: UNIPROT:Q97R83; UNIPARC:UPI0000051655; GB:AE005672; PIDN:AAK75067.
A;Experimental source: strain TIGR4
C;Genetics:
A;Gene: SP0944
C;Superfamily: uridylate kinase

  Query Match 72.5%; Score 37; DB 2; Length 247;
  Best Local Similarity 85.7%; Pred. No. 20;
  Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AGVGSPY 9
 ||:||||
Db 135 AGIGSPY 141

RESULT 8
E97977
UMP kinase (EC 2.7.4.-) [imported] - Streptococcus pneumoniae (strain R6)
C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Accession: E97977
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.;
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.;
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183; 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: E97977
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-247 <KUR>
A;Cross-references: UNIPROT:Q8DQ50; UNIPARC:UPI00000E3531; GB:AE007317; PIDN:AAK99649.
C;Genetics:
A;Gene: pyrH
C;Superfamily: uridylate kinase
C;Keywords: phosphotransferase

  Query Match 72.5%; Score 37; DB 2; Length 247;
  Best Local Similarity 85.7%; Pred. No. 20;
  Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AGVGSPY 9
 ||:||||
Db 135 AGIGSPY 141

RESULT 9
F70780
hypothetical protein Rv0881 - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: F70780
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon,
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd,
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genom
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: F70780
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA

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A;Residues: 1-288 <COL>
A;Cross-references: UNIPROT:Q10543; UNIPARC:UPI0000139DAD; GB:Z73101; GB:AL123456; NID:g
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: Rv0881
C;Superfamily: conserved hypothetical protein HI0860

  Query Match             72.5%;  Score 37;  DB 2;  Length 288;
  Best Local Similarity   75.0%;  Pred. No. 23;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 MAGVGSPY 9
              :||||:||
Db         83 LAGVGAPY 90


RESULT 10
G90450
hypothetical protein SSO2752 [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: G90450
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
 Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: G90450
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-388 <KUR>
A;Cross-references: UNIPROT:Q97V83; UNIPARC:UPI000006483D; GB:AE006641; NID:g13816083; P
C;Genetics:
A;Gene: SSO2752

  Query Match             72.5%;  Score 37;  DB 2;  Length 388;
  Best Local Similarity   60.0%;  Pred. No. 31;
  Matches    6;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              :  |||:|||
Db         16 IKGGVGTPYV 25


RESULT 11
D83679
hypothetical protein BH0236 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: D83679
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: D83679
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1020 <STO>
A;Cross-references: UNIPROT:Q9KG76; UNIPARC:UPI00000C37F3; GB:AP001507; GB:BA000004; NID
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH0236

  Query Match             72.5%;  Score 37;  DB 2;  Length 1020;
  Best Local Similarity   85.7%;  Pred. No. 81;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 GVGSPYV 10
              ||||||:
Db        177 GVGSPYI 183


RESULT 12
T35138
hypothetical protein SC4H8.07c SC4H8.07c - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C;Accession: T35138
R;Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, December 1997
A;Reference number: Z21569
A;Accession: T35138
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-66 <HAR>
A;Cross-references: UNIPROT:O50486; UNIPARC:UPI00000DAB8E; EMBL:AL020958; PIDN:CAA1587
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SC4H8.07c

  Query Match             70.6%;  Score 36;  DB 2;  Length 66;
  Best Local Similarity   75.0%;  Pred. No. 8.2;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSP 8
              |:||:|||
Db         18 VLAGIGSP 25


RESULT 13
D46177
enhancer of split locus protein m3 - fruit fly (Drosophila melanogaster)
N;Alternate names: E(Spl)-HLH-m3; helix-loop-helix protein m3
C;Species: Drosophila melanogaster
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: D46177; D38980; S27814; S28449
R;Delidakis, C.; Artavanis-Tsakonas, S.
Proc. Natl. Acad. Sci. U.S.A. 89, 8731-8735, 1992
A;Title: The Enhancer of split [E(spl)] locus of Drosophila encodes seven independent
A;Reference number: A46177; MUID:92409590; PMID:1528887
A;Accession: D46177
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-224 <DEL>
A;Cross-references: UNIPROT:Q01068; UNIPARC:UPI000000118F; EMBL:M96165; NID:g158490; P
A;Note: sequence extracted from NCBI backbone (NCBIP:114183)
R;Knust, E.; Schrons, H.; Grawe, F.; Campos-Ortega, J.A.
Genetics 132, 505-518, 1992
A;Title: Seven genes of the Enhancer of split complex of Drosophila melanogaster encod
A;Reference number: A38980; MUID:93051287; PMID:1427040
A;Accession: D38980
A;Molecule type: mRNA
A;Residues: 1-149,151-173,'SRR',177-178,180-224 <KNU>
A;Cross-references: UNIPARC:UPI000016BC2C; EMBL:X67046; NID:g8073; PIDN:CAA47431.1; PI
A;Experimental source: strain Oregon R
C;Genetics:
A;Gene: FlyBase:HLHm3
A;Cross-references: FlyBase:FBgn0002609

  Query Match             70.6%;  Score 36;  DB 2;  Length 224;
  Best Local Similarity   87.5%;  Pred. No. 28;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSP 8
              |:||||||
Db         79 VVAGVGSP 86


RESULT 14
WMBEH4
UL34 protein - human herpesvirus 1 (strain 17)
C;Species: human herpesvirus 1
C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 09-Jul-2004
C;Accession: G30085
R;McGeoch, D.J.; Dalrymple, M.A.; Davison, A.J.; Dolan, A.; Frame, M.C.; McNab, D.; Pe
```

J. Gen. Virol. 69, 1531-1574, 1988
A;Title: The complete DNA sequence of the long unique region in the genome of herpes sim
A;Reference number: A30083; MUID:88274327; PMID:2839594
A;Accession: G30085
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-275 <MCG>
A;Cross-references: UNIPROT:P10218; UNIPARC:UPI0000137B9E; GB:X14112; NID:g1944536; PIDN
C;Genetics:
A;Gene: UL34
C;Superfamily: varicella-zoster virus gene 24 protein

  Query Match 70.6%; Score 36; DB 1; Length 275;
  Best Local Similarity 75.0%; Pred. No. 34;
  Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 MAGVGSPY 9
      |||:| ||
Db 1 MAGLGKPY 8

RESULT 15
S65829
hypothetical protein 3 - beet mild yellowing virus
C;Species: beet mild yellowing virus
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997
C;Accession: S65829
R;Guilley, H.; Richards, K.E.; Jonard, G.
Arch. Virol. 140, 1109-1118, 1995
A;Title: Nucleotide sequence of beet mild yellowing virus RNA.
A;Reference number: S65825; MUID:95336315; PMID:7611881
A;Accession: S65829
A;Molecule type: genomic RNA
A;Residues: 1-625 <GUI>
A;Cross-references: UNIPARC:UPI00001757FF; EMBL:X83110
A;Experimental source: isolate 2ITB
A;Note: this reading frame extends between two stop codons and does not begin with a sta
C;Superfamily: potato leaf roll virus RNA-directed RNA polymerase

  Query Match 70.6%; Score 36; DB 2; Length 625;
  Best Local Similarity 87.5%; Pred. No. 77;
  Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 AGVGSPYV 10
      |||| |||
Db 273 AGVGVPYV 280

Search completed: April 11, 2006, 19:35:24
Job time : 40 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 11, 2006, 19:27:40 ; Search time 230 Seconds
(without alignments)
30.675 Million cell updates/sec

Title: US-09-277-064-12
Perfect score: 51
Sequence: 1 VMAGVGSPYV 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	51	100.0	304	2	Q68KJ7_FELCA	Q68kj7 felis silve
2	51	100.0	435	2	Q6ZMM4_HUMAN	Q6zmm4 homo sapien
3	51	100.0	881	2	Q8C0E7_MOUSE	Q8c0e7 m mus muscu
4	51	100.0	1255	1	ERBB2_HUMAN	P04626 homo sapien
5	51	100.0	1257	1	ERBB2_RAT	P06494 rattus norv
6	51	100.0	1259	1	ERBB2_CANFA	O18735 canis famil
7	51	100.0	1259	2	Q8K3F9_RAT	Q8k3f9 rattus norv
8	51	100.0	1305	2	Q6ZPE0_MOUSE	Q6zpe0 mus musculu
9	48	94.1	1254	1	ERBB2_MESAU	Q60553 mesocricetu
10	45	88.2	1275	2	Q5EBY4_BRARE	Q5eby4 brachydanio
11	43	84.3	519	2	Q4HWH3_GIBZE	Q4hwh3 gibberella
12	42	82.4	270	2	Q4T640_TETNG	Q4t640 tetraodon n
13	41	80.4	286	2	Q5JGC5_PYRKO	Q5jgc5 pyrococcus
14	40.5	79.4	63	2	Q4H1F2_HUMAN	Q4h1f2 homo sapien
15	40	78.4	65	2	Q4H1F1_HUMAN	Q4h1f1 homo sapien
16	39	76.5	348	2	Q8LFF9_ARATH	Q8lff9 arabidopsis
17	39	76.5	348	2	Q9M0I6_ARATH	Q9m0i6 arabidopsis
18	39	76.5	465	2	Q523R8_MAGGR	Q523r8 magnaporthe
19	39	76.5	535	2	Q4NMC7_9MICC	Q4nmc7 arthrobacte
20	38	74.5	190	2	Q8KUI3_ACTPA	Q8kui3 actinosynne
21	38	74.5	245	2	Q8DSY1_STRMU	Q8dsy1 streptococc
22	38	74.5	269	2	Q9WWM2_SYNP6	Q9wwm2 synechococc
23	38	74.5	317	2	Q5N0R2_SYNP6	Q5n0r2 synechococc
24	38	74.5	381	1	FTSZ_METTH	O27712 methanobact
25	38	74.5	696	1	SP15_TORCA	P19965 torpedo cal
26	37	72.5	158	2	Q88IB8_PSEPK	Q88ib8 pseudomonas
27	37	72.5	242	1	PYRH_STRP3	P65939 streptococc
28	37	72.5	242	1	PYRH_STRP6	Q5xdh4 streptococc
29	37	72.5	242	1	PYRH_STRP8	P65940 streptococc
30	37	72.5	242	1	PYRH_STRPY	P65938 streptococc
31	37	72.5	242	2	Q8DYG8_STRA5	Q8dyg8 streptococc
32	37	72.5	242	2	Q8E431_STRA3	Q8e431 streptococc
33	37	72.5	245	2	Q5M141_STRT1	Q5m141 streptococc
34	37	72.5	245	2	Q5M5N0_STRT2	Q5m5n0 streptococc
35	37	72.5	246	2	Q4NGD9_9MICC	Q4ngd9 arthrobacte
36	37	72.5	247	1	PYRH_STRPN	Q97r83 streptococc
37	37	72.5	247	1	PYRH_STRR6	Q8dq50 streptococc
38	37	72.5	288	1	Y881_MYCTU	Q10543 mycobacteri
39	37	72.5	288	1	Y905_MYCBO	P59968 mycobacteri
40	37	72.5	296	2	Q8PX83_METMA	Q8px83 methanosarc
41	37	72.5	296	2	Q8TN86_METAC	Q8tn86 methanosarc
42	37	72.5	296	2	Q8TUN5_METAC	Q8tun5 methanosarc
43	37	72.5	388	2	Q97V83_SULSO	Q97v83 sulfolobus
44	37	72.5	389	2	Q7U456_SYNPX	Q7u456 synechococc
45	37	72.5	408	1	FTSZ2_PYRFU	Q8u3e3 pyrococcus

ALIGNMENTS

RESULT 1
Q68KJ7_FELCA
ID Q68KJ7_FELCA PRELIMINARY; PRT; 304 AA.
AC Q68KJ7;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE HER2 (Fragment).
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
OC Felinae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15705889;
RA De Maria R., Olivero M., Iussich S., Nakaichi M., Murata T.,
RA Biolatti B., Di Renzo M.F.;
RT "Spontaneous Feline Mammary Carcinoma Is a Model of HER2
RT Overexpressing Poor Prognosis Human Breast Cancer.";
RL Cancer Res. 65:907-912(2005).
DR EMBL; AY685128; AAU01910.1; -; Genomic_DNA.
DR SMR; Q68KJ7; 57-304.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR008266; Tyr_pkinase_AS.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW ATP-binding; Kinase; Nucleotide-binding; Transferase.
FT NON_TER 1 1
FT NON_TER 304 304
SQ SEQUENCE 304 AA; 33934 MW; 47C0290F4BC020ED CRC64;

Query Match 100.0%; Score 51; DB 2; Length 304;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 VMAGVGSPYV 10
              ||||||||||
Db        126 VMAGVGSPYV 135
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RESULT 2

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Q6ZMM4_HUMAN
ID   Q6ZMM4_HUMAN PRELIMINARY;      PRT;   435 AA.
AC   Q6ZMM4;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein FLJ16821.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Trachea;
RA   Kanehori K., Ishibashi T., Chiba Y., Fujimori K., Hiraoka S.,
RA   Tanai H., Watanabe S., Ishida S., Ono Y., Hotuta T., Watanabe M.,
RA   Sugiyama T., Irie R., Otsuki T., Sato H., Ota T., Wakamatsu A.,
RA   Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
RA   Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA   Wagatsuma M., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
RA   Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
RL   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK131568; BAD18701.1; -; mRNA.
DR   SMR; Q6ZMM4; 254-434.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0005489; F:electron transporter activity; IEA.
DR   GO; GO:0005506; F:iron ion binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0006118; P:electron transport; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR001450; 4Fe4S_ferredoxin.
DR   InterPro; IPR006212; Furin_repeat.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   PRINTS; PR00353; 4FE4SFRDOXIN.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00261; FU; 2.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW   Kinase; Receptor; Tyrosine-protein kinase.
SQ   SEQUENCE   435 AA;  47891 MW;  1FA846710D31311A CRC64;

  Query Match             100.0%;  Score 51;  DB 2;  Length 435;
  Best Local Similarity   100.0%;  Pred. No. 0.46;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db        323 VMAGVGSPYV 332


RESULT 3
Q8C0E7_MOUSE
ID   Q8C0E7_MOUSE PRELIMINARY;      PRT;   881 AA.
AC   Q8C0E7;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Mus musculus 13 days embryo male testis cDNA, RIKEN full-length
DE   enriched library, clone:6030449F08 product:v-erb-b2 erythroblastic
DE   leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene
DE   homolog (avian), full insert sequence. (Fragment).
GN   Name=Erbb2;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Testis;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Testis;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Testis;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Testis;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Testis;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Testis;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
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RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK031542; BAC27442.1; -; mRNA.
DR   HSSP; P06494; 1N8Y.
DR   SMR; Q8C0E7; 1-255.
DR   Ensembl; ENSMUSG00000062312; Mus musculus.
DR   MGI; MGI:95410; Erbb2.
DR   GO; GO:0016324; C:apical plasma membrane; IDA.
DR   GO; GO:0005737; C:cytoplasm; IDA.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0007507; P:heart development; IMP.
DR   GO; GO:0042552; P:myelination; IMP.
DR   GO; GO:0007422; P:peripheral nervous system development; IMP.
DR   InterPro; IPR000494; EGFR_L.
DR   InterPro; IPR006212; Furin_repeat.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   InterPro; IPR004019; YLP_motif.
DR   Pfam; PF01030; Recep_L_domain; 1.
DR   Pfam; PF02757; YLP; 2.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00261; FU; 2.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW   ATP-binding; Kinase; Nucleotide-binding; Transferase;
KW   Tyrosine-protein kinase.
FT   NON_TER       1      1
SQ   SEQUENCE   881 AA;  97501 MW;  5D5042BE9F8F0836 CRC64;

  Query Match           100.0%;  Score 51;  DB 2;  Length 881;
  Best Local Similarity  100.0%;  Pred. No. 0.91;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db        399 VMAGVGSPYV 408


RESULT 4
ERBB2_HUMAN
ID   ERBB2_HUMAN    STANDARD;      PRT;  1255 AA.
AC   P04626; Q14256; Q6LDV1; Q9UMK4;
DT   13-AUG-1987 (Rel. 05, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Receptor tyrosine-protein kinase erbB-2 precursor (EC 2.7.1.112)
DE   (p185erbB2) (C-erbB-2) (NEU proto-oncogene) (Tyrosine kinase-type cell
DE   surface receptor HER2) (MLN 19).
GN   Name=ERBB2; Synonyms=HER2, NEU, NGL;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=86118663; PubMed=3003577;
RA   Yamamoto T., Ikawa S., Akiyama T., Semba K., Nomura N., Miyajima N.,
RA   Saito T., Toyoshima K.;
RT   "Similarity of protein encoded by the human c-erb-B-2 gene to
RT   epidermal growth factor receptor.";
RL   Nature 319:230-234(1986).
RN   [2]
RP   NUCLEOTIDE SEQUENCE, AND VARIANT ALA-1170.
RX   MEDLINE=86070181; PubMed=2999974;
RA   Coussens L., Yang-Feng T.L., Liao Y.C., Chen E., Gray A., McGrath J.,
RA   Seeburg P.H., Libermann T.A., Schlessinger J., Francke U.,
RA   Levinson A., Ullrich A.;
RT   "Tyrosine kinase receptor with extensive homology to EGF receptor
RT   shares chromosomal location with neu oncogene.";
RL   Science 230:1132-1139(1985).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS CYS-452; VAL-655 AND
RP   ALA-1170.
RA   Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W.,
RA   Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
RA   Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
RT   "NIEHS-SNPs, environmental genome project, NIEHS ES15478, Department
RT   of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";
RL   Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   NUCLEOTIDE SEQUENCE OF 1-191.
RX   MEDLINE=87286898; PubMed=3039351;
RA   Tal M., King C.R., Kraus M.H., Ullrich A., Schlessinger J., Givol D.;
RT   "Human HER2 (neu) promoter: evidence for multiple mechanisms for
RT   transcriptional initiation.";
RL   Mol. Cell. Biol. 7:2597-2601(1987).
RN   [5]
RP   NUCLEOTIDE SEQUENCE OF 737-1031.
RX   MEDLINE=86016729; PubMed=2995967;
RA   Semba K., Kamata N., Toyoshima K., Yamamoto T.;
RT   "A v-erbB-related protooncogene, c-erbB-2, is distinct from the c-
RT   erbB-1/epidermal growth factor-receptor gene and is amplified in a
RT   human salivary gland adenocarcinoma.";
RL   Proc. Natl. Acad. Sci. U.S.A. 82:6497-6501(1985).
RN   [6]
RP   NUCLEOTIDE SEQUENCE OF 832-909.
RC   TISSUE=Mammary carcinoma;
RX   MEDLINE=85272597; PubMed=2992089;
RA   King C.R., Kraus M.H., Aaronson S.A.;
RT   "Amplification of a novel v-erbB-related gene in a human mammary
RT   carcinoma.";
RL   Science 229:974-976(1985).
RN   [7]
RP   NUCLEOTIDE SEQUENCE OF 1081-1245, AND VARIANT ALA-1170.
RX   MEDLINE=94000386; PubMed=8104414;
RA   Sarkar F.H., Ball D.E., Li Y.W., Crissman J.D.;
RT   "Molecular cloning and sequencing of an intron of Her-2/neu (ERBB2)
RT   gene.";
RL   DNA Cell Biol. 12:611-615(1993).
RN   [8]
RP   IDENTIFICATION IN A COMPLEX WITH PIK3C2A AND EGFR, IDENTIFICATION IN A
RP   COMPLEX WITH PIK3C2B AND EGFR, AND INTERACTION WITH PIK3C2B.
RX   PubMed=10805725;
RA   Arcaro A., Zvelebil M.J., Wallasch C., Ullrich A., Waterfield M.D.,
RA   Domin J.;
RT   "Class II phosphoinositide 3-kinases are downstream targets of
RT   activated polypeptide growth factor receptors.";
RL   Mol. Cell. Biol. 20:3817-3830(2000).
RN   [9]
RP   INTERACTION WITH PLXNB1.
RX   PubMed=15210733; DOI=10.1083/jcb.200312094;
RA   Swiercz J.M., Kuner R., Offermanns S.;
RT   "Plexin-B1/RhoGEF-mediated RhoA activation involves the receptor
RT   tyrosine kinase ErbB-2.";
RL   J. Cell Biol. 165:869-880(2004).
RN   [10]
RP   X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 654-662 IN COMPLEX WITH HLA
RP   AND BETA-2 MICROGLOBULIN.
RX   MEDLINE=20062861; PubMed=10593938; DOI=10.1074/jbc.274.51.36422;
RA   Kuhns J.J., Batalia M.A., Yan S., Collins E.J.;
RT   "Poor binding of a HER-2/neu epitope (GP2) to HLA-A2.1 is due to a
RT   lack of interactions with the center of the peptide.";
RL   J. Biol. Chem. 274:36422-36427(1999).
RN   [11]
RP   X-RAY CRYSTALLOGRAPHY (2.52 ANGSTROMS) OF 23-629 IN COMPLEX WITH FAB.
RX   MEDLINE=22497871; PubMed=12610629; DOI=10.1038/nature01392;
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RA   Cho H.-S., Mason K., Ramyar K.X., Stanley A.M., Gabelli S.B.,
RA   Denney D.W. Jr., Leahy D.J.;
RT   "Structure of the extracellular region of HER2 alone and in complex
RT   with the Herceptin Fab.";
RL   Nature 421:756-760(2003).
RN   [12]
RP   VARIANTS VAL-654 AND VAL-655.
RX   MEDLINE=93194196; PubMed=8095488;
RA   Ehsani A., Low J., Wallace R.B., Wu A.M.;
RT   "Characterization of a new allele of the human ERBB2 gene by allele-
RT   specific competition hybridization.";
RL   Genomics 15:426-429(1993).
CC   -!- FUNCTION: Essential component of a neuregulin-receptor complex,
CC       althought neuregulins do not interact with it alone. GP30 is a
CC       potential ligand for this receptor. Not activated by EGF, TGF-
CC       alpha and amphiregulin.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- SUBUNIT: Heterodimer with each of the other ERBB receptors
CC       (Potential). Interacts with PRKCABP (By similarity). Binds PLXNB1.
CC       Part of a complex with EGFR and either PIK3C2A or PIK3C2B. May
CC       interact with PIK3C2B when phosphorylated on Tyr-1196.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- PTM: Ligand-binding increases phosphorylation on tyrosine residues
CC       (By similarity).
CC   -!- POLYMORPHISM: There are fours alleles due to the variations in
CC       positions 654 and 655. Allele B1 (Ile-654/Ile-655) has a frequency
CC       of 0.782; allele B2 (Ile-654/Val-655) has a frequency of 0.206;
CC       allele B3 (Val-654/Val-655) has a frequency of 0.012.
CC   -!- SIMILARITY: Belongs to the Tyr protein kinase family. EGF receptor
CC       subfamily.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; M11767; AAA35808.1; -; Genomic_DNA.
DR   EMBL; M11761; AAA35808.1; JOINED; Genomic_DNA.
DR   EMBL; M11762; AAA35808.1; JOINED; Genomic_DNA.
DR   EMBL; M11763; AAA35808.1; JOINED; Genomic_DNA.
DR   EMBL; M11764; AAA35808.1; JOINED; Genomic_DNA.
DR   EMBL; M11765; AAA35808.1; JOINED; Genomic_DNA.
DR   EMBL; M11766; AAA35808.1; JOINED; Genomic_DNA.
DR   EMBL; M11730; AAA75493.1; -; mRNA.
DR   EMBL; M12036; AAA35978.1; -; Genomic_DNA.
DR   EMBL; AY208911; AAO18082.1; -; Genomic_DNA.
DR   EMBL; X03363; CAA27060.1; -; mRNA.
DR   EMBL; M16792; AAA58637.1; -; Genomic_DNA.
DR   EMBL; M16789; AAA58637.1; JOINED; Genomic_DNA.
DR   EMBL; M16790; AAA58637.1; JOINED; Genomic_DNA.
DR   EMBL; M16791; AAA58637.1; JOINED; Genomic_DNA.
DR   EMBL; L29395; AAA35809.1; -; Genomic_DNA.
DR   EMBL; M95667; AAC37531.1; -; Unassigned_DNA.
DR   PIR; A24571; A24571.
DR   PDB; 1N8Z; X-ray; C=23-629.
DR   PDB; 1OVC; Model; A=737-1031.
DR   PDB; 1S78; X-ray; A/B=23-646.
DR   Ensembl; ENSG00000141736; Homo sapiens.
DR   HGNC; HGNC:3430; ERBB2.
DR   MIM; 164870; -.
DR   GO; GO:0016021; C:integral to membrane; NAS.
DR   GO; GO:0005886; C:plasma membrane; NAS.
DR   GO; GO:0005006; F:epidermal growth factor receptor activity; NAS.
DR   GO; GO:0043125; F:ErbB-3 class receptor binding; TAS.
DR   GO; GO:0046982; F:protein heterodimerization activity; NAS.
DR   GO; GO:0004716; F:receptor signaling protein tyrosine kinase . . .; TAS.
DR   GO; GO:0008283; P:cell proliferation; TAS.
DR   GO; GO:0007507; P:heart development; TAS.
DR   GO; GO:0030879; P:mammary gland development; TAS.
DR   GO; GO:0007399; P:neurogenesis; TAS.
DR   GO; GO:0048015; P:phosphoinositide-mediated signaling; NAS.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
DR   GO; GO:0045765; P:regulation of angiogenesis; NAS.
DR   GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; NAS.
DR   InterPro; IPR000494; EGFR_L.
DR   InterPro; IPR006211; Furin-like.
DR   InterPro; IPR006212; Furin_repeat.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   InterPro; IPR004019; YLP_motif.
DR   Pfam; PF00757; Furin-like; 1.
DR   Pfam; PF01030; Recep_L_domain; 2.
DR   Pfam; PF02757; YLP; 2.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00261; FU; 3.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW   3D-structure; ATP-binding; Glycoprotein; Kinase; Multigene family;
KW   Nucleotide-binding; Phosphorylation; Polymorphism; Receptor; Signal;
KW   Transferase; Transmembrane; Tyrosine-protein kinase.
FT   SIGNAL        1     21       Potential.
FT   CHAIN        22   1255       Receptor tyrosine-protein kinase erbB-2.
FT   TOPO_DOM     22    652       Extracellular (Potential).
FT   TRANSMEM    653    675       Potential.
FT   TOPO_DOM    676   1255       Cytoplasmic (Potential).
FT   DOMAIN      720    987       Protein kinase.
FT   NP_BIND     726    734       ATP (By similarity).

  Query Match             100.0%;  Score 51;  DB 1;  Length 1255;
  Best Local Similarity   100.0%;  Pred. No. 1.3;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db        773 VMAGVGSPYV 782


RESULT 5
ERBB2_RAT
ID   ERBB2_RAT      STANDARD;      PRT;  1257 AA.
AC   P06494; Q6P732;
DT   01-JAN-1988 (Rel. 06, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Receptor tyrosine-protein kinase erbB-2 precursor (EC 2.7.1.112)
DE   (p185erbB2) (C-erbB-2) (NEU proto-oncogene) (Epidermal growth factor
DE   receptor-related protein).
GN   Name=Erbb2; Synonyms=Neu;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Neuroblastoma;
RX   MEDLINE=86118662; PubMed=3945311;
RA   Bargmann C.I., Hung M.-C., Weinberg R.A.;
RT   "The neu oncogene encodes an epidermal growth factor receptor-related
RT   protein.";
RL   Nature 319:226-230(1986).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Prostate;
RG   NIH - Mammalian Gene Collection (MGC) project;
RL   Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE OF 634-699.
RX   MEDLINE=92035293; PubMed=1682063;
RA   Masui T., Mann A.M., Macatee T.L., Garland E.M., Okamura T.,
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RA   Smith R.A., Cohen S.M.;
RT   "Direct DNA sequencing of the rat neu oncogene transmembrane domain
RT   reveals no mutation in urinary bladder carcinomas induced by N-butyl-
RT   N-(4-hydroxybutyl)nitrosamine, N-[4-(5-nitro-2-furyl)-2-
RT   thiazolyl]formamide or N-methyl-N-nitrosourea.";
RL   Carcinogenesis 12:1975-1978(1991).
RN   [4]
RP   NUCLEOTIDE SEQUENCE OF 852-905.
RC   TISSUE=Sciatic nerve;
RX   MEDLINE=91222560; PubMed=2025425; DOI=10.1016/0896-6273(91)90167-X;
RA   Lai C., Lemke G.;
RT   "An extended family of protein-tyrosine kinase genes differentially
RT   expressed in the vertebrate nervous system.";
RL   Neuron 6:691-704(1991).
RN   [5]
RP   STRUCTURE BY NMR OF 650-668.
RX   MEDLINE=92155181; PubMed=1346763;
RA   Gullick W.J., Bottomley A.C., Lofts F.J., Doak D.G., Mulvey D.,
RA   Newman R., Crumpton M.J., Sternberg M.J.E., Campbell I.D.;
RT   "Three dimensional structure of the transmembrane region of the proto-
RT   oncogenic and oncogenic forms of the neu protein.";
RL   EMBO J. 11:43-48(1992).
CC   -!- FUNCTION: Essential component of a neuregulin-receptor complex,
CC       althought neuregulins do not interact with it alone. GP30 is a
CC       potential ligand for this receptor. Not activated by EGF, TGF-
CC       alpha and amphiregulin.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- SUBUNIT: Heterodimer with each of the other ERBB receptors. The
CC       constitutively activated oncogenic variant forms a homodimer.
CC       Interacts with PRKCABP and PLXNB1. Part of a complex with EGFR and
CC       either PIK3C2A or PIK3C2B. May interact with PIK3C2B when
CC       phosphorylated on Tyr-1198 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- PTM: Ligand-binding increases phosphorylation on tyrosine residues
CC       (By similarity).
CC   -!- SIMILARITY: Belongs to the Tyr protein kinase family. EGF receptor
CC       subfamily.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; X03362; CAA27059.1; ALT_INIT; mRNA.
DR   EMBL; BC061863; AAH61863.1; ALT_INIT; mRNA.
DR   PIR; A24562; TVRTNU.
DR   PDB; 1N8Y; X-ray; C=23-631.
DR   Ensembl; ENSRNOG00000006450; Rattus norvegicus.
DR   RGD; 2561; Erbb2.
DR   GO; GO:0045595; P:regulation of cell differentiation; TAS.
DR   GO; GO:0042127; P:regulation of cell proliferation; TAS.
DR   InterPro; IPR000494; EGFR_L.
DR   InterPro; IPR006211; Furin-like.
DR   InterPro; IPR006212; Furin_repeat.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   InterPro; IPR004019; YLP_motif.
DR   Pfam; PF00757; Furin-like; 1.
DR   Pfam; PF01030; Recep_L_domain; 2.
DR   Pfam; PF02757; YLP; 2.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00261; FU; 4.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW   3D-structure; ATP-binding; Disease mutation; Glycoprotein; Kinase;
KW   Multigene family; Nucleotide-binding; Phosphorylation; Proto-oncogene;
KW   Receptor; Signal; Transferase; Transmembrane; Tyrosine-protein kinase.
FT   SIGNAL       1     21       Potential.
FT   CHAIN       22   1257       Receptor tyrosine-protein kinase erbB-2.
FT   TOPO_DOM    22    654       Extracellular (Potential).
FT   TRANSMEM   655    677       Potential.
FT   TOPO_DOM   678   1257       Cytoplasmic (Potential).
FT   DOMAIN     722    989       Protein kinase.
FT   NP_BIND    728    736       ATP (By similarity).
FT   REGION    1197   1199       Interaction with PIK3C2B (By similarity).
FT   COMPBIAS   159    369       Cys-rich.
FT   COMPBIAS   473    646       Cys-rich.
FT   ACT_SITE   847    847       By similarity.
FT   BINDING    755    755       ATP (By similarity).
FT   MOD_RES   1141   1141       Phosphotyrosine (by autocatalysis) (By
FT                               similarity).
FT   MOD_RES   1198   1198       Phosphotyrosine (Potential).
FT   MOD_RES   1250   1250       Phosphotyrosine (by autocatalysis) (By
FT                               similarity).
FT   CARBOHYD    68     68       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   188    188       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   260    260       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   532    532       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   573    573       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   631    631       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID   196    205       By similarity.
FT   DISULFID   200    213       By similarity.
FT   DISULFID   221    228       By similarity.
FT   DISULFID   225    236       By similarity.
FT   DISULFID   237    245       By similarity.
FT   DISULFID   241    253       By similarity.
FT   DISULFID   256    265       By similarity.
FT   DISULFID   269    296       By similarity.
FT   DISULFID   300    312       By similarity.
FT   DISULFID   316    332       By similarity.
FT   DISULFID   335    339       By similarity.
FT   DISULFID   513    522       By similarity.
FT   DISULFID   517    530       By similarity.
FT   DISULFID   533    542       By similarity.
FT   DISULFID   546    562       By similarity.
FT   DISULFID   565    578       By similarity.
FT   DISULFID   569    586       By similarity.
FT   DISULFID   589    598       By similarity.
FT   DISULFID   602    625       By similarity.
FT   DISULFID   628    636       By similarity.
FT   DISULFID   632    644       By similarity.
FT   VARIANT    661    661       V -> E (in oncogenic NEU).
FT   CONFLICT   145    145       S -> G (in Ref. 2).
FT   CONFLICT   505    509       LCVSS -> CGLE (in Ref. 2).
SQ   SEQUENCE   1257 AA;  138832 MW;  6129264583011402 CRC64;

  Query Match             100.0%;  Score 51;  DB 1;  Length 1257;
  Best Local Similarity   100.0%;  Pred. No. 1.3;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db        775 VMAGVGSPYV 784


RESULT 6
ERBB2_CANFA
ID   ERBB2_CANFA     STANDARD;      PRT;  1259 AA.
AC   O18735;
DT   25-OCT-2004 (Rel. 45, Created)
DT   25-OCT-2004 (Rel. 45, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Receptor tyrosine-protein kinase erbB-2 precursor (EC 2.7.1.112)
DE   (p185erbB2) (C-erbB-2).
GN   Name=ERBB2;
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC   Canis.
OX   NCBI_TaxID=9615;
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RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Mammary gland;
RA   Yokota H.;
RT   "cDNA cloning of erbB-2 from canine mammary gland.";
RL   Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Essential component of a neuregulin-receptor complex,
CC       althought neuregulins do not interact with it alone. GP30 is a
CC       potential ligand for this receptor. Not activated by EGF, TGF-
CC       alpha and amphiregulin (By similarity).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- SUBUNIT: Heterodimer with each of the other ERBB receptors
CC       (Potential). Interacts with PRKCABP. Binds PLXNB1. Part of a
CC       complex with EGFR and either PIK3C2A or PIK3C2B. May interact with
CC       PIK3C2B when phosphorylated on Tyr-1200 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- PTM: Ligand-binding increases phosphorylation on tyrosine residues
CC       (By similarity).
CC   -!- SIMILARITY: Belongs to the Tyr protein kinase family. EGF receptor
CC       subfamily.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; AB008451; BAA23127.1; -; mRNA.
DR   HSSP; P04626; 1N8Z.
DR   SMR; O18735; 23-628.
DR   Ensembl; ENSCAFG00000016351; Canis familiaris.
DR   InterPro; IPR000494; EGFR_L.
DR   InterPro; IPR006211; Furin-like.
DR   InterPro; IPR006212; Furin_repeat.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   InterPro; IPR004019; YLP_motif.
DR   Pfam; PF00757; Furin-like; 1.
DR   Pfam; PF01030; Recep_L_domain; 2.
DR   Pfam; PF02757; YLP; 2.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00261; FU; 3.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW   ATP-binding; Glycoprotein; Kinase; Multigene family;
KW   Nucleotide-binding; Phosphorylation; Receptor; Signal; Transferase;
KW   Transmembrane; Tyrosine-protein kinase.
FT   SIGNAL        1     22       Potential.
FT   CHAIN        23   1259       Receptor tyrosine-protein kinase erbB-2.
FT   TOPO_DOM     23    653       Extracellular (Potential).
FT   TRANSMEM    654    674       Potential.
FT   TOPO_DOM    675   1259       Cytoplasmic (Potential).
FT   DOMAIN      719    986       Protein kinase.
FT   NP_BIND     725    733       ATP (By similarity).
FT   REGION     1199   1201       Interaction with PIK3C2B (By similarity).
FT   COMPBIAS    192    268       Cys-rich.
FT   COMPBIAS   1101   1219       Pro-rich.
FT   ACT_SITE    844    844       By similarity.
FT   BINDING     752    752       ATP (By similarity).
FT   MOD_RES    1138   1138       Phosphotyrosine (by autocatalysis) (By
FT                                similarity).
FT   MOD_RES    1200   1200       Phosphotyrosine (Potential).
FT   MOD_RES    1252   1252       Phosphotyrosine (by autocatalysis) (By
FT                                similarity).
FT   CARBOHYD     68     68       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    259    259       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    421    421       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    529    529       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    570    570       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    628    628       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID    195    204       By similarity.
FT   DISULFID    199    212       By similarity.
FT   DISULFID    220    227       By similarity.
FT   DISULFID    224    235       By similarity.
FT   DISULFID    236    244       By similarity.
FT   DISULFID    240    252       By similarity.
FT   DISULFID    255    264       By similarity.
FT   DISULFID    268    295       By similarity.
FT   DISULFID    299    311       By similarity.
FT   DISULFID    315    331       By similarity.
FT   DISULFID    334    338       By similarity.
FT   DISULFID    511    519       By similarity.
FT   DISULFID    514    527       By similarity.
FT   DISULFID    530    539       By similarity.
FT   DISULFID    543    559       By similarity.
FT   DISULFID    562    575       By similarity.
FT   DISULFID    566    583       By similarity.
FT   DISULFID    586    595       By similarity.
FT   DISULFID    599    622       By similarity.
FT   DISULFID    625    633       By similarity.
FT   DISULFID    629    641       By similarity.
SQ   SEQUENCE   1259 AA;  137991 MW;  E37364D49C4ACD46 CRC64;

  Query Match             100.0%;  Score 51;  DB 1;  Length 1259;
  Best Local Similarity   100.0%;  Pred. No. 1.3;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db        772 VMAGVGSPYV 781


RESULT 7
Q8K3F9_RAT
ID   Q8K3F9_RAT  PRELIMINARY;      PRT;  1259 AA.
AC   Q8K3F9;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Neu protooncoprotein.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=BDIX;
RA   Watson P.A., Kim K., Chen K.-S., Gould M.N.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY116182; AAM50093.1; -; mRNA.
DR   HSSP; P06494; 1N8Y.
DR   SMR; Q8K3F9; 26-633.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0005006; F:epidermal growth factor receptor activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.
DR   InterPro; IPR002048; EF-hand.
DR   InterPro; IPR000494; EGFR_L.
DR   InterPro; IPR006211; Furin-like.
DR   InterPro; IPR006212; Furin_repeat.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   InterPro; IPR004019; YLP_motif.
DR   Pfam; PF00757; Furin-like; 1.
DR   Pfam; PF01030; Recep_L_domain; 2.
DR   Pfam; PF02757; YLP; 2.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
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DR   SMART; SM00261; FU; 4.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
SQ   SEQUENCE   1259 AA;  139101 MW;  B724BD5CC33AE953 CRC64;

  Query Match             100.0%;  Score 51;  DB 2;  Length 1259;
  Best Local Similarity   100.0%;  Pred. No. 1.3;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db        777 VMAGVGSPYV 786


RESULT 8
Q6ZPE0_MOUSE
ID   Q6ZPE0_MOUSE PRELIMINARY;      PRT;  1305 AA.
AC   Q6ZPE0;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   MKIAA3023 protein (Fragment).
GN   Name=Erbb2; Synonyms=mKIAA3023;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Embryonic tail;
RX   MEDLINE=22977043; PubMed=14621295;
RA   Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
RA   Saga Y., Nagase T., Ohara O., Koga H.;
RT   "Prediction of the coding sequences of mouse homologues of KIAA gene:
RT   III. the complete nucleotide sequences of 500 mouse KIAA-homologous
RT   cDNAs identified by screening of terminal sequences of cDNA clones
RT   randomly sampled from size-fractionated libraries.";
RL   DNA Res. 10:167-180(2003).
DR   EMBL; AK129487; BAC98297.1; -; mRNA.
DR   HSSP; P11362; 1AGW.
DR   SMR; Q6ZPE0; 72-679.
DR   Ensembl; ENSMUSG00000062312; Mus musculus.
DR   MGI; MGI:95410; Erbb2.
DR   GO; GO:0016324; C:apical plasma membrane; IDA.
DR   GO; GO:0005737; C:cytoplasm; IDA.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0007507; P:heart development; IMP.
DR   GO; GO:0042552; P:myelination; IMP.
DR   GO; GO:0007422; P:peripheral nervous system development; IMP.
DR   InterPro; IPR000494; EGFR_L.
DR   InterPro; IPR006211; Furin-like.
DR   InterPro; IPR006212; Furin_repeat.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   InterPro; IPR004019; YLP_motif.
DR   Pfam; PF00757; Furin-like; 1.
DR   Pfam; PF01030; Recep_L_domain; 2.
DR   Pfam; PF02757; YLP; 2.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00261; FU; 4.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW   ATP-binding; Kinase; Nucleotide-binding; Transferase.
FT   NON_TER       1      1
SQ   SEQUENCE   1305 AA;  143508 MW;  A51D897408521860 CRC64;

  Query Match             100.0%;  Score 51;  DB 2;  Length 1305;
  Best Local Similarity   100.0%;  Pred. No. 1.3;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db        823 VMAGVGSPYV 832


RESULT 9
ERBB2_MESAU
ID   ERBB2_MESAU    STANDARD;      PRT;  1254 AA.
AC   Q60553;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Receptor tyrosine-protein kinase erbB-2 precursor (EC 2.7.1.112)
DE   (p185erbB2) (C-erbB-2) (NEU proto-oncogene).
GN   Name=ERBB2; Synonyms=NEU;
OS   Mesocricetus auratus (Golden hamster).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Cricetidae; Cricetinae; Mesocricetus.
OX   NCBI_TaxID=10036;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Nerve;
RX   MEDLINE=94193007; PubMed=7908275; DOI=10.1016/0378-1119(94)90553-3;
RA   Nakamura T., Ushijima T., Ishizaka Y., Nagao M., Arai M., Yamazaki Y.,
RA   Ishikawa T.;
RT   "Cloning and activation of the Syrian hamster neu proto-oncogene.";
RL   Gene 140:251-255(1994).
CC   -!- FUNCTION: Essential component of a neuregulin-receptor complex,
CC       althought neuregulins do not interact with it alone. GP30 is a
CC       potential ligand for this receptor. Not activated by EGF, TGF-
CC       alpha and amphiregulin (By similarity).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- SUBUNIT: Heterodimer with each of the other ERBB receptors
CC       (Potential). Part of a complex with EGFR and either PIK3C2A or
CC       PIK3C2B. Interacts with PRKCABP and PLXNB1. May interact with
CC       PIK3C2B when phosphorylated on Tyr-1196 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- PTM: Ligand-binding increases phosphorylation on tyrosine
CC       residues.
CC   -!- SIMILARITY: Belongs to the Tyr protein kinase family. EGF receptor
CC       subfamily.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; D16295; BAA03801.1; -; mRNA.
DR   PIR; I48161; I48161.
DR   HSSP; P06494; 1N8Y.
DR   SMR; Q60553; 23-629.
DR   InterPro; IPR000494; EGFR_L.
DR   InterPro; IPR006211; Furin-like.
DR   InterPro; IPR006212; Furin_repeat.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   InterPro; IPR004019; YLP_motif.
DR   Pfam; PF00757; Furin-like; 1.
DR   Pfam; PF01030; Recep_L_domain; 2.
DR   Pfam; PF02757; YLP; 2.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
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DR   SMART; SM00261; FU; 4.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW   ATP-binding; Disease mutation; Glycoprotein; Kinase; Multigene family;
KW   Nucleotide-binding; Phosphorylation; Proto-oncogene; Receptor; Signal;
KW   Transferase; Transmembrane; Tyrosine-protein kinase.
FT   SIGNAL       1     21       Potential.
FT   CHAIN       22   1254       Receptor tyrosine-protein kinase erbB-2.
FT   TOPO_DOM    22    652       Extracellular (Potential).
FT   TRANSMEM   653    675       Potential.
FT   TOPO_DOM   676   1254       Cytoplasmic (Potential).
FT   DOMAIN     720    987       Protein kinase.
FT   NP_BIND    726    734       ATP (By similarity).
FT   REGION    1195   1197       Interaction with PIK3C2B (By similarity).
FT   COMPBIAS   158    368       Cys-rich.
FT   COMPBIAS   472    644       Cys-rich.
FT   ACT_SITE   845    845       By similarity.
FT   BINDING    753    753       ATP (By similarity).
FT   MOD_RES   1139   1139       Phosphotyrosine (by autocatalysis) (By
FT                               similarity).
FT   MOD_RES   1196   1196       Phosphotyrosine (Potential).
FT   MOD_RES   1247   1247       Phosphotyrosine (by autocatalysis) (By
FT                               similarity).
FT   CARBOHYD    68     68       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   125    125       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   187    187       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   259    259       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   530    530       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   571    571       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   629    629       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID   195    204       By similarity.
FT   DISULFID   199    212       By similarity.
FT   DISULFID   236    244       By similarity.
FT   DISULFID   240    252       By similarity.
FT   DISULFID   255    264       By similarity.
FT   DISULFID   268    295       By similarity.
FT   DISULFID   299    311       By similarity.
FT   DISULFID   315    331       By similarity.
FT   DISULFID   334    338       By similarity.
FT   DISULFID   511    520       By similarity.
FT   DISULFID   515    528       By similarity.
FT   DISULFID   531    540       By similarity.
FT   DISULFID   544    560       By similarity.
FT   DISULFID   563    576       By similarity.
FT   DISULFID   567    584       By similarity.
FT   DISULFID   587    596       By similarity.
FT   DISULFID   600    623       By similarity.
FT   DISULFID   626    634       By similarity.
FT   DISULFID   630    642       By similarity.
FT   VARIANT    658    658       V -> E (in oncogenic NEU).
FT   VARIANT    659    659       V -> E (in oncogenic NEU).
SQ   SEQUENCE  1254 AA;  138253 MW;  974C3791C21F2BE1 CRC64;

  Query Match             94.1%;  Score 48;  DB 1;  Length 1254;
  Best Local Similarity   90.0%;  Pred. No. 4.8;
  Matches    9;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||:|||||
Db        773 VMAGLGSPYV 782


RESULT 10
Q5EBY4_BRARE
ID   Q5EBY4_BRARE PRELIMINARY;      PRT;  1275 AA.
AC   Q5EBY4;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Erbb2.
GN   Name=erbb2; ORFNames=zgc:63601;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=15797019;
RA   Lyons D.A., Pogoda H.M., Voas M.G., Woods I.G., Diamond B., Nix R.,
RA   Arana N., Jacobs J., Talbot W.S.;
RT   "erbb3 and erbb2 Are Essential for Schwann Cell Migration and
RT   Myelination in Zebrafish.";
RL   Curr. Biol. 15:513-524(2005).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Pogoda H.-M., Voas M.G., Talbot W.S.;
RT   "Analysis of a zebrafish erbb2 gene.";
RL   Submitted (JAN-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY914799; AAX09341.1; -; mRNA.
DR   ZFIN; ZDB-GENE-031118-121; zgc:63601.
DR   InterPro; IPR000494; EGFR_L.
DR   InterPro; IPR006211; Furin-like.
DR   InterPro; IPR006212; Furin_repeat.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF00757; Furin-like; 1.
DR   Pfam; PF00069; Pkinase; 1.
DR   Pfam; PF01030; Recep_L_domain; 2.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00261; FU; 3.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
SQ   SEQUENCE  1275 AA;  140828 MW;  67462B4F1B68492F CRC64;

  Query Match             88.2%;  Score 45;  DB 2;  Length 1275;
  Best Local Similarity   90.0%;  Pred. No. 19;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||| ||||
Db        766 VMAGVASPYV 775


RESULT 11
Q4HWH3_GIBZE
ID   Q4HWH3_GIBZE PRELIMINARY;      PRT;  519 AA.
AC   Q4HWH3;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Hypothetical protein.
GN   ORFNames=FG10685.1;
OS   Gibberella zeae PH-1.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
OX   NCBI_TaxID=229533;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=PH-1;
RA   Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
RA   Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavkiy L.,
RA   Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA   Choepel Y., Collymore A., Cook A., Cooke P., Corum B., DeArellano K.,
RA   Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA   Erickson J., Faro S., Ferreira P., FitzGerald M., Gage D., Galagan J.,
RA   Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
RA   Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
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RA   Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
RA   Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
RA   Ma L.-J., Mabbitt R., MacLean C., Macdonald P., Major J., Manning J.,
RA   Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,
RA   Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
RA   Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neil D.,
RA   Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
RA   Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
RA   Roman J., Schauer S., Schupback R., Seaman S., Severy P., Smirnov S.,
RA   Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
RA   Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,
RA   Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA   Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
RA   Lander E.;
RT   "Fusarium graminearum genome sequence.";
RL   Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AACM01000446; EAA70307.1; -; Genomic_DNA.
KW   Hypothetical protein.
SQ   SEQUENCE   519 AA;  57083 MW;  4E4CE0E4972A2FA9 CRC64;

  Query Match           84.3%;  Score 43;  DB 2;  Length 519;
  Best Local Similarity  70.0%;  Pred. No. 19;
  Matches    7;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              |:||||:||:
Db        142 VVAGVGAPYI 151


RESULT 12
Q4T640_TETNG
ID   Q4T640_TETNG PRELIMINARY;      PRT;   270 AA.
AC   Q4T640;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Chromosome undetermined SCAF8938, whole genome shotgun sequence.
DE   (Fragment).
GN   ORFNames=GSTENG00006492001;
OS   Tetraodon nigroviridis (Green puffer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Tetraodon.
OX   NCBI_TaxID=99883;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA   Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA   Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA   Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA   Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA   Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA   Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA   Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA   Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
RA   Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA   Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA   Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
RT   "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT   the early vertebrate proto-karyotype.";
RL   Nature 431:946-957(2004).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RG   Genoscope; Whitehead Institute Centre for Genome Research;
RL   Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; CAAE01008938; CAF91642.1; -; Genomic_DNA.
FT   NON_TER       1      1
SQ   SEQUENCE   270 AA;  30448 MW;  29F922C1476C58A8 CRC64;

  Query Match           82.4%;  Score 42;  DB 2;  Length 270;
  Best Local Similarity  90.0%;  Pred. No. 16;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              |||||| ||
Db        126 VMAGVGSMYV 135


RESULT 13
Q5JGC5_PYRKO
ID   Q5JGC5_PYRKO PRELIMINARY;      PRT;   286 AA.
AC   Q5JGC5;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Probable fumarate hydratase, alpha subunit.
GN   OrderedLocusNames=TK1965;
OS   Pyrococcus kodakaraensis (Thermococcus kodakaraensis).
OC   Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC   Thermococcus.
OX   NCBI_TaxID=69014;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=KOD1;
RX   PubMed=15710748; DOI=10.1101/gr.3003105;
RA   Fukui T., Atomi H., Kanai T., Matsumi R., Fujiwara S., Imanaka T.;
RT   "Complete genome sequence of the hyperthermophilic archaeon
RT   Thermococcus kodakaraensis KOD1 and comparison with Pyrococcus
RT   genomes.";
RL   Genome Res. 15:352-363(2005).
DR   EMBL; AP006878; BAD86154.1; -; Genomic_DNA.
DR   GO; GO:0016829; F:lyase activity; IEA.
DR   InterPro; IPR004646; TtdA_fumA_fumB.
DR   Pfam; PF05681; Fumerase; 1.
DR   TIGRFAMs; TIGR00722; ttdA_fumA_fumB; 1.
KW   Complete proteome.
SQ   SEQUENCE   286 AA;  30729 MW;  DA4E5B901438EC65 CRC64;

  Query Match           80.4%;  Score 41;  DB 2;  Length 286;
  Best Local Similarity  70.0%;  Pred. No. 26;
  Matches    7;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              | ||:||||:
Db         71 VKAGIGSPYL 80


RESULT 14
Q4H1F2_HUMAN
ID   Q4H1F2_HUMAN PRELIMINARY;      PRT;    63 AA.
AC   Q4H1F2;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   ERBB2 (Fragment).
GN   Name=ERBB2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Yamanaka S., Sato M., Fujisaki R., Sakurada A., Inoue A., Nukiwa T.,
RA   Kondo T., Horii A.;
RT   "Exploration of siRNA Targeting EGFR as a Candidate for a Novel
RT   Therapeutic Application in Lung Cancer.";
RL   Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB221349; BAE15959.1; -; Genomic_DNA.
```

```
FT   NON_TER       1      1
FT   NON_TER      63     63
SQ   SEQUENCE   63 AA;  6927 MW;  EE62C915FB7B6D6A CRC64;

  Query Match             79.4%;  Score 40.5;  DB 2;  Length 63;
  Best Local Similarity   90.9%;  Pred. No. 7.5;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 VMAGV-GSPYV 10
              ||||| |||||
Db          4 VMAGVGGSPYV 14


RESULT 15
Q4H1F1_HUMAN
ID   Q4H1F1_HUMAN PRELIMINARY;      PRT;    65 AA.
AC   Q4H1F1;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   ERBB2 (Fragment).
GN   Name=ERBB2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Yamanaka S., Sato M., Fujisaki R., Sakurada A., Inoue A., Nukiwa T.,
RA   Kondo T., Horii A.;
RT   "Exploration of siRNA Targeting EGFR as a Candidate for a Novel
RT   Therapeutic Application in Lung Cancer.";
RL   Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB221350; BAE15960.1; -; Genomic_DNA.
FT   NON_TER       1      1
FT   NON_TER      65     65
SQ   SEQUENCE   65 AA;  7111 MW;  BF169BFB4415620F CRC64;

  Query Match             78.4%;  Score 40;  DB 2;  Length 65;
  Best Local Similarity   100.0%;  Pred. No. 9.7;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSP 8
              ||||||||
Db          4 VMAGVGSP 11


Search completed: April 11, 2006, 19:34:40
Job time : 233 secs
```

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 11, 2006, 19:15:04 ; Search time 184 Seconds
(without alignments)
23.879 Million cell updates/sec

Title: US-09-277-064-12
Perfect score: 51
Sequence: 1 VMAGVGSPYV 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 556551

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	51	100.0	10	2	AAR61525	Aar61525 Peptide f
2	51	100.0	10	2	AAR97508	Aar97508 Cytotoxic
3	51	100.0	10	2	AAW36826	Aaw36826 Immunogen
4	51	100.0	10	2	AAW70071	Aaw70071 HER-2/neu
5	51	100.0	10	2	AAW77132	Aaw77132 HER-2/neu
6	51	100.0	10	4	AAB99690	Aab99690 HLA A2 bi
7	51	100.0	10	4	AAG89003	Aag89003 HER2/neu
8	51	100.0	10	4	AAG88772	Aag88772 HER2/neu
9	51	100.0	10	5	ABB76755	Abb76755 Tumour an
10	51	100.0	10	5	AAE26800	Aae26800 Human HLA
11	51	100.0	10	5	AEA36306	Aea36306 Human HER
12	51	100.0	10	6	ABU63012	Abu63012 Human Her
13	51	100.0	10	8	ADE97756	Ade97756 Immunogen
14	51	100.0	10	8	ADM12647	Adm12647 MHC class
15	51	100.0	10	8	ADO38880	Ado38880 Human Her
16	51	100.0	10	8	ADP79761	Adp79761 Human HLA
17	47	92.2	9	2	AAY46001	Aay46001 Immunogen
18	47	92.2	9	2	AAY46413	Aay46413 Immunogen
19	47	92.2	9	2	AAY46478	Aay46478 Immunogen
20	47	92.2	9	4	AAG88305	Aag88305 HER2/NEU
21	47	92.2	9	4	AAE12134	Aae12134 Human HER
22	47	92.2	9	8	ADP79931	Adp79931 Human HLA
23	47	92.2	10	2	AAY37958	Aay37958 Human cER
24	47	92.2	10	2	AAY45527	Aay45527 Immunogen
25	41	80.4	9	4	AAG88941	Aag88941 HER2/neu
26	41	80.4	9	7	ADG38697	Adg38697 Human Her
27	41	80.4	9	7	ADW30548	Adw30548 HLA bindi
28	41	80.4	9	7	ADW30664	Adw30664 HLA bindi
29	41	80.4	9	8	ADP79932	Adp79932 Human HLA
30	40	78.4	9	4	AAG88321	Aag88321 HER2/NEU
31	32	62.7	9	4	AAG88503	Aag88503 HER2/NEU
32	29	56.9	8	4	AAM23398	Aam23398 HIV pepti
33	29	56.9	9	2	AAW30834	Aaw30834 TRP-2 der
34	29	56.9	9	4	AAM23323	Aam23323 HIV pepti
35	29	56.9	9	4	ABP14007	Abp14007 HIV A02 s
36	29	56.9	9	4	ABP19510	Abp19510 HIV B62 s
37	29	56.9	10	4	ABP14013	Abp14013 HIV A02 s
38	29	56.9	10	4	ABP18334	Abp18334 HIV B58 s
39	29	56.9	10	4	ABP16406	Abp16406 HIV A24 s
40	29	56.9	10	7	ADN14184	Adn14184 HIV B cel
41	29	56.9	10	8	ADN64625	Adn64625 HLA bindi
42	29	56.9	10	8	ADP80235	Adp80235 Human HLA
43	28	54.9	8	4	AAM22702	Aam22702 HIV pepti
44	28	54.9	8	4	AAM22701	Aam22701 HIV pepti
45	27	52.9	10	4	AAG93812	Aag93812 Human com

ALIGNMENTS

RESULT 1
AAR61525
ID AAR61525 standard; peptide; 10 AA.
XX
AC AAR61525;
XX
DT 25-MAR-2003 (revised)
DT 11-MAY-1995 (first entry)
XX
DE Peptide fragment (1.0738) of c-ERB2 binds HLA-A2.1.
XX
KW antigen; epitope; immunogenic target protein; PSA; HBVc; HBVs; EBV; HIV1;
KW plasma specific antigen; hepatitis B virus; Epstein Barr;
KW human immunodeficiency virus; human papilloma virus; p53; c-ERB2; MAGE-1;
KW melanoma antigen-1; core antigen; surface antigen;
KW pharmaceutical composition; in vivo; ex vivo; therapeutic; diagnostic;
KW MHC class I molecule; major histocompatability complex; HLA-A2.1; 9mer;
KW 10mer; anchor; human leukocyte antigen.
XX
OS Homo sapiens.
XX
PN WO9420127-A1.
XX
PD 15-SEP-1994.
XX
PF 04-MAR-1994; 94WO-US002353.
XX
PR 05-MAR-1993; 93US-00027146.
PR 04-JUN-1993; 93US-00073205.
PR 29-NOV-1993; 93US-00159184.
XX
PA (CYTE-) CYTEL CORP.
XX
PI Grey HM, Sette A, Sidney J, Kast W;
XX
DR WPI; 1994-302678/37.
XX
PT Immunogenic peptide(s) having an HLA-A2.1 binding motif - used for
PT treatment or prophylaxis of cancer, virus infection or autoimmune
PT diseases.
XX
PS Example 5; Page 108; 138pp; English.
XX
CC AAR59496-R61666 are immunogenic 10mer peptides that contain a HLA-A2.1
CC binding motif. These peptides bind HLA-A2.1 and have a binding affinity
CC of at least 1% as compared to a reference peptide (AAR71293). AAR61525
CC has an IC50 of 0.018 and the sequence occurs at position 773 in the human

```
CC   c-ERB2 gene product. Peptides of the invention can induce cytotoxic T
CC   lymphocytes which can react with target cells. They can be used for the
CC   treatment or prophlyaxis of cancer, eg. prostate cancer or lymphoma, etc.
CC   (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 10 AA;

  Query Match           100.0%;  Score 51;  DB 2;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0.013;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db          1 VMAGVGSPYV 10


RESULT 2
AAR97508
ID   AAR97508 standard; peptide; 10 AA.
XX
AC   AAR97508;
XX
DT   11-FEB-1997 (first entry)
XX
DE   Cytotoxic T lymphocyte-activating Her-2/Neu-specific peptide.
XX
KW   p53; Her-2; Neu; aa; amino acid; CTL; cytotoxic T lymphocyte; target;
KW   malignant cell; antigenic; vaccine; immunisation; activation.
XX
OS   Homo sapiens.
XX
PN   WO9618409-A1.
XX
PD   20-JUN-1996.
XX
PF   14-DEC-1995;   95WO-US016415.
XX
PR   14-DEC-1994;   94US-00355558.
XX
PA   (SCRI ) SCRIPPS RES INST.
XX
PI   Sherman LA;
XX
DR   WPI; 1996-300385/30.
XX
PT   In vivo activation of tumour-specific cytotoxic T lymphocytes - by
PT   contacting with polypeptide(s) derived from human p53 or Her-2/Neu
PT   proteins.
XX
PS   Claim 5; Page 124; 158pp; English.
XX
CC   AAR97508 is a peptide capable of activating cytotoxic T lymphocytes
CC   (CTLs) which specifically target malignant cells. The peptide corresponds
CC   to amino acids 773-782 of human Her-2/Neu protein. CTL- activating
CC   peptides can be used in a vaccine for protecting against tumour cell
CC   formation. CTLs activated by the peptides will lyse tumour cells
CC   displaying specific peptides. Antibodies against CTL- activating peptides
CC   are useful for the identification of other similar compounds which may be
CC   useful for treating cancer or virally- infected cells, or for diagnosis.
CC   The peptide and vaccines produced provide immunity to a high percentage
CC   of different ethnic groups, i.e. those with different HLA alleles
XX
SQ   Sequence 10 AA;

  Query Match           100.0%;  Score 51;  DB 2;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0.013;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db          1 VMAGVGSPYV 10


RESULT 3
AAW36826
ID   AAW36826 standard; peptide; 10 AA.
XX
AC   AAW36826;
XX
DT   23-MAR-1998  (first entry)
XX
DE   Immunogenic peptide H7 based on the human Her-2/neu protein.
XX
KW   Her-2/neu protein; human leukocyte antigen A2.1; HLA;
KW   cytotoxic T lymphocyte; CTL; immune response; tumour-associated antigen;
KW   T-cell receptor; TCR; tumour treatment.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9732603-A1.
XX
PD   12-SEP-1997.
XX
PF   05-MAR-1997;   97WO-US003611.
XX
PR   05-MAR-1996;   96US-0012845P.
XX
PA   (SCRI ) SCRIPPS RES INST.
XX
PI   Sherman LA,  Lustgarten J;
XX
DR   WPI; 1997-470496/43.
XX
PT   Nucleic acid encoding variable regions of HLA-restricted non-human T cell
PT   receptor specific for tumour antigen - used to identify tumour antigens
PT   and for tumour therapy.
XX
PS   Example 1; Page 9; 34pp; English.
XX
CC   Synthetic peptides AAW36824-40 are based on the sequence of the human Her
CC   -2/neu protein, wherein each sequence contains the anchor motif for human
CC   leukocyte antigen (HLA) A2.1. The present peptide is based on positions
CC   773-782. The ability of these peptides to inhibit the binding of an
CC   influenza virus matrix protein peptide M1 to HLA A2.1 was measured by
CC   inhibition of lysis by an M1 specific, HLA A2.1 restricted, cytotoxic T
CC   lymphocyte (CTL) clone. The present protein showed 55% inhibition. The
CC   peptides were also tested for their ability to elicit an immune response
CC   in vivo. However, only H3 (AAW36824) and H7 (AAW36826) were able to do
CC   this. H3 and H7 peptides are tumour-associated antigens, and were used to
CC   immunize a transgenic, non-human vertebrate (that has been modified to
CC   express at least one HLA antigen), so that the animal produces CTL which
CC   displays HLA-restricted T-cell receptor (TCR) specificity for the
CC   antigen. Nucleic acid encoding variable regions of the alpha and beta
CC   chains of such TCRs can be amplified from CTLs produced in the above
CC   manner. Cells expressing recombinant TCR are used to identify antigens
CC   associated with a tumour and to treat tumours in humans. Transgenic mice
CC   are a more convenient source of CTL than the tumour-infiltrating
CC   lymphocytes previously used. TCR can be humanised to reduce side-
CC   reactions and short peptide derivatives of TCR are more economical to
CC   produce than TCR itself, particularly when expressed as a single-chain
CC   molecule rather than as a dimer
XX
SQ   Sequence 10 AA;

  Query Match           100.0%;  Score 51;  DB 2;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0.013;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db          1 VMAGVGSPYV 10


RESULT 4
AAW70071
```

ID AAW70071 standard; peptide; 10 AA.
XX
AC AAW70071;
XX
DT 22-OCT-1998 (first entry)
XX
DE HER-2/neu derived HLA-A2.1 binding peptide 19 (residues 773-782).
XX
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
KW human leukocyte antigen; HLA; tumour associated antigen; cancer;
KW antigen presenting cell; APC; immunogenic peptide; immune disorder;
KW viral infection; AIDS; hepatitis; bacterial infection; malaria;
KW fungal infection; tuberculosis; melanoma; HER-2/neu; cerB-2.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9833888-A1.
XX
PD 06-AUG-1998.
XX
PF 30-JAN-1998; 98WO-US001959.
XX
PR 31-JAN-1997; 97US-0036696P.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Tsai V, Southwood S, Sidney J, Sette A, Celis E;
XX
DR WPI; 1998-437445/37.
XX
PT Production of antigen-specific cytotoxic T cells - by incubating
PT immunogenic peptide(s) from antigen that binds class I major
PT histocompatibility complex molecules with pre-treated antigen presenting
PT cells.
XX
PS Example 7; Page 77; 104pp; English.
XX
CC Sequences shown in AAW70053 to AAW70075 represent peptides derived from
CC HER-2/neu (cerB-2) antigen. The peptides can bind to a human leukocyte
CC antigen (HLA), HLA-A2.1 and are used to exemplify the method of invention
CC of producing antigen-specific cytotoxic T cells (CTLs) in vitro. The
CC method comprises contacting immunogenic peptides from an antigen that
CC binds class I major histocompatibility complex (MHC) molecules with
CC antigen presenting cells (APCs) pretreated with pretreatment growth
CC factors, and incubating the APCs with purified CD8 cells in the presence
CC of at least 2 incubation growth factors, thereby producing antigen-
CC specific CTLs. A method for specifically killing target cells in a human
CC patient is also provided which comprises obtaining a fluid sample
CC containing CTLs from a patient, contacting the cytotoxic T cells with
CC APCs pretreated with pre-treatment growth factors, where the APCs
CC comprise class I MHC molecules. The pretreated APCs are incubated with
CC the cytotoxic growth factors, thereby producing activated CTLs which are
CC contacted with a carrier to form a composition. The composition can then
CC be administered to the patient. The activated CTLs can be used for
CC treating cancers, immune disorders, viral infections, AIDS, hepatitis,
CC bacterial infection, fungal infection, malaria or tuberculosis
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 51; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VMAGVGSPYV 10
||||||||||
Db 1 VMAGVGSPYV 10

RESULT 5
AAW77132
ID AAW77132 standard; peptide; 10 AA.
XX
AC AAW77132;
XX
DT 16-NOV-1998 (first entry)
XX
DE HER-2/neu synthetic peptide epitope 2.
XX
KW Tyrosinase; tyrosinase cytotoxic lymphocyte response;
KW cytotoxic T lymphocyte; cysteine-depleted; melanoma.
XX
OS Synthetic.
XX
PN WO9833810-A2.
XX
PD 06-AUG-1998.
XX
PF 29-JAN-1998; 98WO-US001592.
XX
PR 30-JAN-1997; 97US-0037781P.
XX
PA (UYVI-) UNIV VIRGINIA PATENT FOUND.
XX
PI Slingluff CL, Hunt DF, Engelhard VH, Kittlesen D;
XX
DR WPI; 1998-437388/37.
XX
PT Disease specific immunogen - comprises disease specific cytotoxic T
PT lymphocyte epitope used to elicit melanoma specific CTL response.
XX
PS Disclosure; Page 27; 93pp; English.
XX
CC The peptide epitope AAW77119-W77138 were created for human tumour-
CC specific cytotoxic T lymphocyte response. These peptides are are cysteine
CC - depleted mutants of a native disease-specific CTL epitope. The cysteine
CC - depleted CTL epitopes elicit a stronger or more specific CTL response
CC than the native epitope. The epitopes can be used in a disease-specific
CC immunogen to protect a mammal against disease in particular melanomas.
CC The peptides may also be used to screen a sample for the presence of an
CC antigen with the same epitope, or with a different cross-reactive epitope
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 51; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VMAGVGSPYV 10
||||||||||
Db 1 VMAGVGSPYV 10

RESULT 6
AAB99690
ID AAB99690 standard; peptide; 10 AA.
XX
AC AAB99690;
XX
DT 06-SEP-2001 (first entry)
XX
DE HLA A2 binding CTL epitope peptide from Her2/neu SEQ ID NO:11.
XX
KW Human leukocyte antigen A2 binding peptide; HLA class I A2; CTL;
KW cytotoxic T-cell lymphocyte; tumour associated antigen; CEA; HER2/neu;
KW MAGE2; MAGE3; p53; vaccine; cancer; cytostatic; immunomodulator;
KW immunotherapy; immune response.
XX
OS Homo sapiens.
XX
PN WO200141741-A1.
XX
PD 14-JUN-2001.
XX
PF 13-DEC-2000; 2000WO-US034318.
XX

PR 13-DEC-1999; 99US-0170448P.
PR 05-APR-2000; 2000US-00543608.
PR 30-MAY-2000; 2000US-00583200.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Fikes J, Sette A, Sidney J, Southwood S, Celis E, Keogh E;
PI Chesnut R;
XX
DR WPI; 2001-381489/40.
XX
PT Compositions for use in a vaccine for treating, e.g., breast, lung and
PT colon cancer comprises at least one peptide that comprises an isolated
PT epitope of a tumor-associated antigen.
XX
PS Claim 1; Page 76; 86pp; English.
XX
CC The present invention describes a composition (I) comprising at least one
CC peptide that comprises an isolated, prepared epitope consisting of a
CC sequence selected from 25 short amino acid sequences given in AAB99680 to
CC AAB99704. Also described are: (1) a composition (II) comprising one or
CC more peptides, and further comprising at least two epitopes selected from
CC the 25 short amino acid sequences (as above), where each of the one or
CC more peptides comprise less than 50 contiguous amino acids that have 100%
CC identity with a native peptide sequence; and (2) a vaccine composition
CC (III) comprising an epitope selected from the 25 short amino acid
CC sequences (as above) and a pharmaceutical excipient. (I) has cytostatic
CC and immunomodulatory activities and can be used in vaccine production and
CC immunotherapy. The peptide epitope compositions (I)-(II) are useful for
CC monitoring an immune response to a tumour associated antigen or when one
CC or more peptides are combined to create a vaccine (III) that stimulates
CC the cellular arm of the immune system. In particular, the vaccine
CC mediates immune responses against tumours in individuals who bear an
CC allele of the human leukocyte antigen (HLA)-A2 supertype and improve the
CC standard of care for patients being treated for breast, colon, or lung
CC cancer
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 51; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VMAGVGSPYV 10
||||||||||
Db 1 VMAGVGSPYV 10

RESULT 7
AAG89003
ID AAG89003 standard; peptide; 10 AA.
XX
AC AAG89003;
XX
DT 11-SEP-2001 (first entry)
XX
DE HER2/neu epitope HLA-A2 supermotif-bearing peptide #16.
XX
KW Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;
KW immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;
KW tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200141787-A1.
XX
PD 14-JUN-2001.
XX
PF 11-DEC-2000; 2000WO-US033591.
XX
PR 10-DEC-1999; 99US-00458299.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;
PI Keogh E;
XX
DR WPI; 2001-374995/39.
XX
PT An isolated prepared HER2/neu epitope useful in a vaccine for inducing
PT cellular immune responses for the prevention and treatment of cancer.
XX
PS Claim 1; Page 189; 199pp; English.
XX
CC The present invention describes isolated prepared HER2/neu epitopes (I).
CC Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is
CC culture in vitro and binds to a complex of an epitope (I), bound to a
CC human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)
CC and a second epitope and the peptide is less than 50 contiguous amino
CC acids that have 100% identity with a native peptide sequence of HER2/neu;
CC (3) a vaccine composition (III) comprising (II) and a pharmaceutical
CC excipient; (4) an isolated nucleic acid encoding a peptide comprising (I)
CC ; and (5) an isolated nucleic acid encoding (II). (I) has cytostatic and
CC immunostimulant activities, and can be used in vaccines. (I), (II) and
CC (III) are useful for inducing cellular immune responses for the
CC prevention and treatment of cancer. (I) and (II) are useful for
CC monitoring or evaluating an immune response to a tumour-associated
CC antigen when incubated with a T lymphocyte sample form a patient and
CC detecting the presence of bound T lymphocyte to (I) or (II). Epitope
CC based vaccines mean that immunosuppressive epitopes that may be present
CC in whole antigens may be avoided. Selected epitopes may be combined to
CC enhance immunogenicity. The possible pathological side effects caused by
CC infectious agents or whole protein antigen is eliminated. The vaccine
CC provides the ability to direct and focus an immune response to multiple
CC selected antigens from the same pathogen. Epitope-based anti-tumour
CC vaccines provides the opportunity to combine epitopes derived from
CC multiple tumour-associated molecules addressing the problem of tumour-
CC tumour variability and reducing the likelihood of tumour escape due to
CC antigen loss. AAG88266 to AAG89121 represent amino acid sequences used in
CC the exemplification of the present invention
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 51; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VMAGVGSPYV 10
||||||||||
Db 1 VMAGVGSPYV 10

RESULT 8
AAG88772
ID AAG88772 standard; peptide; 10 AA.
XX
AC AAG88772;
XX
DT 11-SEP-2001 (first entry)
XX
DE HER2/neu A2 supermotif crossbinding peptide #16.
XX
KW Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;
KW immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;
KW tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200141787-A1.
XX
PD 14-JUN-2001.
XX
PF 11-DEC-2000; 2000WO-US033591.
XX

PR 10-DEC-1999; 99US-00458299.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;
PI Keogh E;
XX
DR WPI; 2001-374995/39.
XX
PT An isolated prepared HER2/neu epitope useful in a vaccine for inducing
PT cellular immune responses for the prevention and treatment of cancer.
XX
PS Example 2; Page 179; 199pp; English.
XX
CC The present invention describes isolated prepared HER2/neu epitopes (I).
CC Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is
CC culture in vitro and binds to a complex of an epitope (I), bound to a
CC human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)
CC and a second epitope and the peptide is less than 50 contiguous amino
CC acids that have 100% identity with a native peptide sequence of HER2/neu;
CC (3) a vaccine composition (III) comprising (II) and a pharmaceutical
CC excipient; (4) an isolated nucleic acid encoding a peptide comprising (I)
CC ; and (5) an isolated nucleic acid encoding (II). (I) has cytostatic and
CC immunostimulant activities, and can be used in vaccines. (I), (II) and
CC (III) are useful for inducing cellular immune responses for the
CC prevention and treatment of cancer. (I) and (II) are useful for
CC monitoring or evaluating an immune response to a tumour-associated
CC antigen when incubated with a T lymphocyte sample form a patient and
CC detecting the presence of bound T lymphocyte to (I) or (II). Epitope
CC based vaccines mean that immunosuppressive epitopes that may be present
CC in whole antigens may be avoided. Selected epitopes may be combined to
CC enhance immunogenicity. The possible pathological side effects caused by
CC infectious agents or whole protein antigen is eliminated. The vaccine
CC provides the ability to direct and focus an immune response to multiple
CC selected antigens from the same pathogen. Epitope-based anti-tumour
CC vaccines provides the opportunity to combine epitopes derived from
CC multiple tumour-associated molecules addressing the problem of tumour-
CC tumour variability and reducing the likelihood of tumour escape due to
CC antigen loss. AAG88266 to AAG89121 represent amino acid sequences used in
CC the exemplification of the present invention
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 51; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VMAGVGSPYV 10
||||||||||
Db 1 VMAGVGSPYV 10

RESULT 9
ABB76755
ID ABB76755 standard; peptide; 10 AA.
XX
AC ABB76755;
XX
DT 31-MAY-2002 (first entry)
XX
DE Tumour antigen epitope HER-2/neu 773 presented by HLA A2.1.
XX
KW Antiviral; anti-HIV; cytostatic; epitope; HLA A2.1;
KW human leukocyte antigen; immunotherapy; cancer; viral infection; vaccine.
XX
OS Unidentified.
XX
PN FR2812087-A1.
XX
PD 25-JAN-2002.
XX
PF 21-JUL-2000; 2000FR-00009591.
XX
PR 21-JUL-2000; 2000FR-00009591.
XX
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
XX
PI Kosmatopoulos K, Tourdot S, Scardino A, Gross DA;
XX
DR WPI; 2002-189846/25.
XX
PT Identifying subdominant or cryptic epitopes, useful in immunotherapy of
PT cancer and viral infection, comprises testing modified, non-immunogenic
PT peptides for induction of cytotoxic T cells.
XX
PS Example 1; Page 12; 62pp; French.
XX
CC The present invention relates to subdominant/cryptic epitopes that are
CC presented by HLA (human leukocyte antigen) Class I molecule A2.1. The
CC epitopes or chimeric polypeptides containing them and nucleic acid
CC encoding them are useful for preventative or curative immunotherapy of
CC cancer and viral infections, particularly where used as vaccines. The
CC present peptide was used to illustrate the invention
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 51; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VMAGVGSPYV 10
||||||||||
Db 1 VMAGVGSPYV 10

RESULT 10
AAE26800
ID AAE26800 standard; peptide; 10 AA.
XX
AC AAE26800;
XX
DT 13-DEC-2002 (first entry)
XX
DE Human HLA-A2.1 restricted HER-2/neu peptide epitope #6.
XX
KW Human; cancer; breast cancer; ovarian cancer; melanoma; cell therapy;
KW epitope; human leucocyte antigen; HLA-A2.1.
XX
OS Homo sapiens.
XX
PN WO200265992-A2.
XX
PD 29-AUG-2002.
XX
PF 19-FEB-2002; 2002WO-US005748.
XX
PR 20-FEB-2001; 2001US-0270252P.
XX
PA (ORTH) ORTHO-MCNEIL PHARM INC.
XX
PI Degraw J, Moriarty A, Leturcq DJ, Jackson MR, Peterson PA;
PI Heiskala M;
XX
DR WPI; 2002-667033/71.
XX
PT Treating a subject with cancer comprises combining the CD+8 cells, which
PT are stimulated with non-naturally occurring antigen-presenting cell line,
PT with adherent blood monocytes and inoculating the subject with CD8+
PT suspension.
XX
PS Example 2; Page 92; 99pp; English.
XX
CC The invention relates to a method of treating a subject with cancer. The
CC method involves combining the CD+8 cells, which are stimulated with non
CC naturally occurring antigen-presenting cell (nnAPC) line, with adherent
CC blood monocytes and inoculating the subject with CD8+ suspension. The

```
CC   method is useful for treating cancer e.g. ovarian cancer, breast cancer
CC   and melanoma etc. It is also useful in cell therapy. The present sequence
CC   is human leukocyte antigen A2 (HLA-A2).1 restricted peptide epitope used
CC   to treat breast and ovarian cancer
XX
SQ   Sequence 10 AA;

  Query Match          100.0%;  Score 51;  DB 5;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0.013;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db          1 VMAGVGSPYV 10


RESULT 11
AEA36306
ID   AEA36306 standard; peptide; 10 AA.
XX
AC   AEA36306;
XX
DT   11-AUG-2005  (first entry)
XX
DE   Human HER-2/neu 773-782 cytotoxic T-lymphocyte epitope peptide.
XX
KW   viral infection; virucide; cytostatic; tumor; neoplasm; cell therapy;
KW   antigen; HER-2/neu.
XX
OS   Homo sapiens.
XX
PN   JP2005139118-A.
XX
PD   02-JUN-2005.
XX
PF   07-NOV-2003; 2003JP-00377653.
XX
PR   20-FEB-2001; 2001US-0270252P.
XX
PA   (ORTH ) ORTHO-MCNEIL PHARM INC.
XX
PI   Leturco DJ,  Moriarty AM,  Jackson MR,  Peterson PA,  Richards JM;
XX
DR   WPI; 2002-667033/71.
XX
PT   Treating a subject with cancer comprises combining the CD+8 cells, which
PT   are stimulated with non-naturally occurring antigen-presenting cell line,
PT   with adherent blood monocytes and inoculating the subject with CD8+
PT   suspension.
XX
PS   Example 3; SEQ ID NO 16; 65pp; Japanese.
XX
CC   The invention relates to a novel method for treating viral infection in a
CC   subject. The method comprises preparing an antigen presentation cell
CC   lineage (nnAPC), collecting CD8+ cells from the subject, stimulating CD8+
CC   cells using the nnAPC, culturing CD8+ cells in the presence of
CC   interleukin-2 (IL-2) and/or IL-7, mixing peripheral blood monocytes from
CC   the subject, subjecting the components to gamma irradiation, combining
CC   the CD8+ cells with adhesive peripheral blood monocytes and inoculating
CC   the CD8+ suspended solid to the subject. The method of the invention
CC   demonstrates virucide and cytostatic activities and may be useful for
CC   treating a viral infection or tumor in a subject via cell therapy. The
CC   current sequence is that of a human HER-2/neu cytotoxic T-lymphocyte
CC   epitope peptide of the invention which was incorporated into a Drosophila
CC   antigen presenting cell.
XX
SQ   Sequence 10 AA;

  Query Match          100.0%;  Score 51;  DB 5;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0.013;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db          1 VMAGVGSPYV 10


RESULT 12
ABU63012
ID   ABU63012 standard; peptide; 10 AA.
XX
AC   ABU63012;
XX
DT   16-SEP-2003  (first entry)
XX
DE   Human Her-2/Neu-derived CTL epitope HER-7.
XX
KW   CTL; cytotoxic C lymphocyte; epitope; p53; cytostatic; anti-tumour;
KW   virucide; immunosuppressive; vaccine; human; immune response;
KW   tumour-associated antigen; cancer; tumour; neoplasm; viral infection;
KW   retroviral infection; autoimmune response; Her-2; Neu.
XX
OS   Homo sapiens.
XX
PN   US2003064916-A1.
XX
PD   03-APR-2003.
XX
PF   26-MAR-1999;   99US-00277064.
XX
PR   08-AUG-1997;   97US-00860232.
XX
PA   (SHER/) SHERMAN L A.
XX
PI   Sherman LA;
XX
DR   WPI; 2003-512514/48.
XX
PT   Novel polypeptide useful for activating cytotoxic T lymphocytes in vivo
PT   which are useful in the diagnosis and treatment of variety of disease
PT   conditions such as cancer, tumors, and neoplasia.
XX
PS   Claim 5; Page 52; 77pp; English.
XX
CC   The invention relates to a polypeptide capable of specifically activating
CC   cytotoxic T lymphocytes (CTLs) in vivo which can then specifically target
CC   malignant cells, or having substantial homology with a CTL epitope, or
CC   its sequential subsets. Also included are a population of specific
CC   cytotoxic T cells capable of lysing tumour cells displaying a specific
CC   peptide, a vaccine comprising an immunogenically effective amount of CTL-
CC   stimulating peptide, generating activated CTL cells in vivo, generating
CC   CTL cells that will target a specific population of cells, specifically
CC   killing target cells in an individual using specific, activated CTLs,
CC   provoking an immune response to a tumour-associated antigen, identifying
CC   specific CTLs responsive to a specific T cell epitope, detecting specific
CC   CTLs having receptors capable of binding a specific T cell epitope in a
CC   tissue sample, detecting anti-p53 antibodies in an individual, an
CC   antibody molecule that immunoreacts with the polypeptide and a hybridoma
CC   capable of secreting the above antibodies. The methods are useful for
CC   specifically killing target cells in an individual using specific,
CC   activated CTLs and the polypeptide is useful for provoking an immune
CC   response to a tumour-associated antigen in mammal and the reaction occurs
CC   in vitro. The CTL epitope peptide is useful for activating CTLs in vivo
CC   with specificity for particular antigenic peptides, and these activated
CC   CTLs are useful in the diagnosis and treatment of variety of disease
CC   conditions such as cancer, tumours, neoplasia, viral and retroviral
CC   infections, and autoimmune response. The present sequence is a CTL
CC   epitope of the invention derived from the tumour associated antigen Her-
CC   2/Neu
XX
SQ   Sequence 10 AA;

  Query Match          100.0%;  Score 51;  DB 6;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0.013;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          1 VMAGVGSPYV 10
              ||||||||||
Db          1 VMAGVGSPYV 10


RESULT 13
ADE97756
ID   ADE97756 standard; peptide; 10 AA.
XX
AC   ADE97756;
XX
DT   12-FEB-2004  (first entry)
XX
DE   Immunogenic HLA-A2.1 binding peptide #238.
XX
KW   cytostatic; anti-inflammatory; hepatotropic; virucide; anti-HIV;
KW   nephrotropic; neuroprotective; antiarthritic; antirheumatic;
KW   immunosuppressive; dermatological; muscular; nephrotropic; thyromimetic;
KW   haemostatic; antithyroid; antianaemic; anabolic; hypertensive;
KW   immunogenic peptide composition; immune response; prostate cancer;
KW   hepatitis B; hepatitis C; AIDS; renal carcinoma; cervical carcinoma;
KW   lymphoma; cytomegalovirus; CMV; condlylloma acuminatum;
KW   autoimmune associated disorder; multiple sclerosis; rheumatoid arthritis;
KW   Sjogren syndrome; scleroderma; polymyositis; dermatomyositis;
KW   systemic lupus erythematosus; juvenile rheumatoid arthritis;
KW   ankylosing spondylitis; myasthenia gravis; MG; bullous pemphigoid;
KW   pemphigus; glomerulonephritis; Goodpasture's syndrome;
KW   autoimmune haemolytic anaemia; Hashimoto's disease; pernicious anaemia;
KW   idiopathic thrombocytopenic purpura; Grave's disease; Addison's disease;
KW   human leukocyte anitgen A2.1; HLA A2.1;
KW   immunogenic HLA-A2.1 binding peptide.
XX
OS   Synthetic.
XX
PN   US2003185822-A1.
XX
PD   02-OCT-2003.
XX
PF   03-APR-2002; 2002US-00116557.
XX
PR   05-MAR-1993;   93US-00027146.
PR   04-JUN-1993;   93US-00073205.
PR   29-NOV-1993;   93US-00159184.
PR   02-DEC-1994;   94US-00349177.
XX
PA   (GREY/) GREY H M.
PA   (SETT/) SETTE A.
PA   (SIDN/) SIDNEY J.
XX
PI   Grey HM,  Sette A,  Sidney J;
XX
DR   WPI; 2004-041186/04.
XX
PT   Immunogenic peptide composition for preventing, treating or diagnosing
PT   pathological states, e.g. prostate cancer, hepatitis B and C, Acquired
PT   Immunodeficiency Syndrome, and renal carcinoma, includes conserved
PT   residues at specified positions.
XX
PS   Example 11; Page 25; 38pp; English.
XX
CC   The invention describes an immunogenic peptide composition comprising 9
CC   residues including a first conserved residue at a second position from N-
CC   terminus, and a second conserved residue at C-terminal position. The
CC   inventive peptide composition is used to elicit an immune response
CC   against a desired antigen for preventing, treating or diagnosing
CC   pathological states, e.g. prostate cancer, hepatitis B, hepatitis C,
CC   AIDS, renal carcinoma, cervical carcinoma, lymphoma, cytomegalovirus
CC   (CMV), and condlylloma acuminatum. It is also used to treat autoimmune
CC   associated disorders, e.g. multiple sclerosis, rheumatoid arthritis,
CC   Sjogren syndrome, scleroderma, polymyositis, dermatomyositis, systemic
CC   lupus erythematosus, juvenile rheumatoid arthritis, ankylosing
CC   spondylitis, myasthenia gravis (MG), bullous pemphigoid, pemphigus,
CC   glomerulonephritis, Goodpasture's syndrome, autoimmune hemolytic anemia,
CC   Hashimoto's disease, pernicious anaemia, idiopathic thrombocytopenic
CC   purpura, Grave's disease, and Addison's disease. The invention defines
CC   positions within a motif enabling the selection of the peptides, which
CC   will bind efficiently to human leukocyte anitgen (HLA) A2.1. This is the
CC   amino acid sequence of an immunogenic HLA-A2.1 binding peptide.
XX
SQ   Sequence 10 AA;

  Query Match             100.0%;  Score 51;  DB 8;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.013;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db          1 VMAGVGSPYV 10


RESULT 14
ADM12647
ID   ADM12647 standard; peptide; 10 AA.
XX
AC   ADM12647;
XX
DT   20-MAY-2004  (first entry)
XX
DE   MHC class I epitope of human Her-2/neu, 16-6-9.
XX
KW   antigen presentation enhancing hybrid polypeptide; mammalian Ii-Key;
KW   MHC class II; antibacterial; virucide; fungicide; antirheumatic;
KW   antiarthritic; neuroprotective; dermatological; immunosuppressive;
KW   antiinflammatory; antidiabetic; antithyroid; immune;
KW   rheumatoid arthritis; multiple sclerosis; lupus erythematosus;
KW   diabetes mellitus; myasthenia gravis; autoimmune thyroiditis;
KW   scleroderma; dermatomyositis; pemphigus.
XX
OS   Homo sapiens.
XX
PN   US2003235594-A1.
XX
PD   25-DEC-2003.
XX
PF   17-SEP-2002; 2002US-00245871.
XX
PR   14-SEP-1999;   99US-00396813.
PR   17-JUL-2002; 2002US-00197000.
XX
PA   (ANTI-) ANTIGEN EXPRESS INC.
XX
PI   Humphreys R,  Xu M;
XX
DR   WPI; 2004-070554/07.
XX
PT   Novel Ii-Key/antigen presentation enhancing hybrid polypeptide, useful
PT   for treating infections, rheumatoid arthritis, multiple sclerosis, lupus
PT   erythematosus and diabetes mellitus.
XX
PS   Example 16; Page 55; 87pp; English.
XX
CC   The invention relates to a novel antigen presentation enhancing hybrid
CC   polypeptide. The novel polypeptide has an N-terminal element consisting
CC   of 4-16 residues of a mammalian Ii-Key peptide and its non-N-terminal
CC   deletion modifications, a chemical structure covalently linking the N-
CC   terminal elelment to an MHC class II-presented epitope of a C-terminal
CC   element. The C-terminal element comprises an antigenic epitope, which
CC   binds to an antigenic peptide binding site of an MHC class II molecule.
CC   The antigen presentation enhancing hybrid polypeptide has the following
CC   activities: antibacterial, virucide, fungicide, antirheumatic,
CC   antiarthritic, neuroprotective, dermatological, immunosuppressive,
CC   antiinflammatory, antidiabetic, and antithyroid. The antigen presentation
CC   enhancing hybrid polypeptide is useful for modulating the immune response
CC   in an individual and for treating infections (such as bacteria, virus,
CC   parasite and fungus), rheumatoid arthritis, multiple sclerosis, lupus
CC   erythematosus, diabetes mellitus, myasthenia gravis, autoimmune
```

CC thyroiditis, scleroderma, dermatomyositis and pemphigus. This sequence
CC represents a mammalian Ii key related peptide epitope of the invention.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 51; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VMAGVGSPYV 10
||||||||||
Db 1 VMAGVGSPYV 10

RESULT 15
ADO38880
ID ADO38880 standard; peptide; 10 AA.
XX
AC ADO38880;
XX
DT 15-JUL-2004 (first entry)
XX
DE Human Her-2/neu MHC class II-presented epitope #67.
XX
KW Antibacterial; Virucide; Fungicide; Antiparasitic; Antiarthritic;
KW Antirheumatic; Neuroprotective; Antiinflammatory; Dermatological;
KW Immunosuppressive; Antidiabetic; Antithyroid; Antiasthmatic;
KW Antiallergic; Cytostatic; Antipsoriatic; Gene Therapy; Vaccine;
KW MHC Class II; Ii-key motif; immune response; anthrax; EBOLA; HIV;
KW influenza; vaccinia virus; infection; bacterium; virus; parasite; fungus;
KW rickettsia; rheumatoid arthritis; multiple sclerosis;
KW lupus erythematosus; diabetes mellitus; myasthenia gravis;
KW autoimmune thyroiditis; scleroderma; dermatomyositis; pemphigus; asthma;
KW allergic rhinitis; topical dermatitis; colitis; cancer; psoriasis;
KW adenoma.
XX
OS Homo sapiens.
XX
PN US2004058881-A1.
XX
PD 25-MAR-2004.
XX
PF 24-SEP-2002; 2002US-00253286.
XX
PR 24-SEP-2002; 2002US-00253286.
XX
PA (ANTI-) ANTIGEN EXPRESS INC.
XX
PI Humphreys RE, Xu M;
XX
DR WPI; 2004-294259/27.
XX
PT New non-naturally occurring protein or polypeptide modified by
PT recombinant DNA techniques, useful for treating multiple sclerosis,
PT diabetes mellitus, myasthenia gravis, scleroderma, allergic rhinitis,
PT colitis, cancer or psoriasis.
XX
PS Example 16; Page 57; 90pp; English.
XX
CC The invention relates to a non-naturally occurring protein or polypeptide
CC (I) modified by recombinant DNA techniques comprising: a C-terminal
CC element comprising an MHC Class II-presented epitope; an N-terminal
CC element comprising an Ii-key motif; and an intervening element comprising
CC a sequence of 4-11 amino acid residues where the modification by
CC recombinant DNA techniques taking place within elements (b) and (c). Also
CC described are methods for: suppressing or enhancing an immune response
CC directed toward an MHC (major histocompatibility complex) Class II-
CC presented epitope of interest. Suppressing an immune response directed
CC toward an MHC Class II-presented epitope of interest comprises: providing
CC a nucleic acid sequence encoding the MHC Class II-presented epitope of
CC interest, the nucleic acid sequence encoding an Ii-Key motif located 4-11
CC amino acids upstream from the N-terminal residue of the MHC Class II-
CC presented epitope of interest; and modifying the Ii-Key motif to decrease
CC its conformance to the archetypal Ii-Key regulatory motif. Enhancing an
CC immune response directed toward an MHC Class II-presented epitope of
CC interest comprises: providing a nucleic acid sequence encoding the MHC
CC Class II-presented epitope of interest, the nucleic acid sequence lacking
CC an Ii-key motif located 4-11 amino acids upstream from the N-terminal
CC residue of the MHC Class II-presented epitope of interest; and modifying
CC the nucleic acid sequence to introduce an Ii-key motif appropriately
CC spaced from the MHC Class II-presented epitope. The protein or
CC polypeptide of interest corresponds to a protein or polypeptide encoded
CC by an infectious pathogen selected from anthrax, EBOLA, HIV or influenza,
CC preferably vaccinia virus. The non-naturally occurring protein or
CC polypeptide (I) modified by recombinant DNA techniques is useful for
CC treating infectious diseases caused or associated with infection by a
CC bacterium, virus, parasite, fungus, rickettsia or other infectious
CC agents. It is also useful for treating rheumatoid arthritis, multiple
CC sclerosis, lupus erythematosus, diabetes mellitus, myasthenia gravis,
CC autoimmune thyroiditis, scleroderma, dermatomyositis, pemphigus, asthma,
CC allergic rhinitis, topical dermatitis, colitis, cancer, psoriasis or
CC adenomas. The present sequence represents the amino acid sequence of an
CC MHC class II-presented epitope used in the invention.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 51; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VMAGVGSPYV 10
||||||||||
Db 1 VMAGVGSPYV 10

Search completed: April 11, 2006, 19:18:40
Job time : 187 secs

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Title: US-09-277-064-12
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Sequence: 1 VMAGVGSPYV 10

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Maximum DB seq length: 10

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Maximum Match 100%
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SUMMARIES

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1	51	100.0	10	1	US-08-467-083-29	Sequence 29, Appl
2	51	100.0	10	1	US-08-414-417B-29	Sequence 29, Appl
3	51	100.0	10	1	US-08-486-348A-29	Sequence 29, Appl
4	51	100.0	10	1	US-08-468-545B-29	Sequence 29, Appl
5	51	100.0	10	2	US-08-466-680B-29	Sequence 29, Appl
6	51	100.0	10	2	US-09-341-982-95	Sequence 95, Appl
7	51	100.0	10	2	US-09-543-608A-16	Sequence 16, Appl
8	51	100.0	10	2	US-09-354-533-29	Sequence 29, Appl
9	51	100.0	10	4	PCT-US95-16415-12	Sequence 12, Appl
10	47	92.2	9	2	US-09-527-487-9	Sequence 9, Appli
11	47	92.2	10	2	US-08-159-339A-263	Sequence 263, App
12	29	56.9	9	1	US-08-725-736D-10	Sequence 10, Appl
13	29	56.9	9	2	US-09-162-368B-10	Sequence 10, Appl
14	29	56.9	9	2	US-09-161-877B-10	Sequence 10, Appl
15	27	52.9	10	1	US-08-172-707-5	Sequence 5, Appli
16	27	52.9	10	1	US-08-412-865-5	Sequence 5, Appli
17	27	52.9	10	1	US-08-476-505-5	Sequence 5, Appli
18	27	52.9	10	1	US-08-487-396-5	Sequence 5, Appli
19	27	52.9	10	1	US-08-941-553-5	Sequence 5, Appli
20	27	52.9	10	2	US-08-769-143-5	Sequence 5, Appli
21	26	51.0	9	1	US-08-725-736D-9	Sequence 9, Appli
22	26	51.0	9	2	US-09-162-368B-9	Sequence 9, Appli
23	26	51.0	9	2	US-09-162-368B-28	Sequence 28, Appl
24	26	51.0	9	2	US-09-161-877B-9	Sequence 9, Appli
25	26	51.0	9	2	US-09-161-877B-28	Sequence 28, Appl
26	25	49.0	8	2	US-09-082-737-12	Sequence 12, Appl
27	25	49.0	8	2	US-09-718-032-12	Sequence 12, Appl
28	25	49.0	9	1	US-08-725-736D-8	Sequence 8, Appli
29	25	49.0	9	1	US-08-725-736D-14	Sequence 14, Appl
30	25	49.0	9	1	US-08-318-856A-36	Sequence 36, Appl
31	25	49.0	9	2	US-09-162-368B-8	Sequence 8, Appli
32	25	49.0	9	2	US-09-162-368B-14	Sequence 14, Appl
33	25	49.0	9	2	US-09-162-368B-31	Sequence 31, Appl
34	25	49.0	9	2	US-09-161-877B-8	Sequence 8, Appli
35	25	49.0	9	2	US-09-161-877B-14	Sequence 14, Appl
36	25	49.0	9	2	US-09-161-877B-31	Sequence 31, Appl
37	25	49.0	10	2	US-09-100-930A-14	Sequence 14, Appl
38	24	47.1	7	2	US-08-861-153A-28	Sequence 28, Appl
39	24	47.1	8	2	US-09-239-043D-4	Sequence 4, Appli
40	24	47.1	8	2	US-09-239-043D-1321	Sequence 1321, Ap
41	24	47.1	9	1	US-08-725-736D-4	Sequence 4, Appli
42	24	47.1	9	1	US-08-725-736D-7	Sequence 7, Appli
43	24	47.1	9	1	US-08-725-736D-11	Sequence 11, Appl
44	24	47.1	9	2	US-08-880-963-8	Sequence 8, Appli
45	24	47.1	9	2	US-09-162-368B-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-08-467-083-29
; Sequence 29, Application US/08467083
; Patent No. 5726023
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,083
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/414,417
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; TELEX: 3723836 SEEDANBERRY
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-467-083-29

Query Match 100.0%; Score 51; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0097;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 VMAGVGSPYV 10
              ||||||||||
Db          1 VMAGVGSPYV 10


RESULT 2
US-08-414-417B-29
; Sequence 29, Application US/08414417B
; Patent No. 5801005
;  GENERAL INFORMATION:
;    APPLICANT:  Cheever, Martin A.
;    APPLICANT:  Disis, Mary L.
;    TITLE OF INVENTION:  IMMUNE REACTIVITY TO HER-2/neu PROTEIN
;    TITLE OF INVENTION:  FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
;    TITLE OF INVENTION:  HER-2/neu ONCOGENE IS ASSOCIATED
;    NUMBER OF SEQUENCES:  69
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed and Berry LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  US
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/414,417B
;      FILING DATE:  31-MAR-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sharkey, Richard G.
;      REGISTRATION NUMBER:  32,629
;      REFERENCE/DOCKET NUMBER:  920010.448C2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  29:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
US-08-414-417B-29

  Query Match             100.0%;  Score 51;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.0097;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db          1 VMAGVGSPYV 10


RESULT 3
US-08-486-348A-29
; Sequence 29, Application US/08486348A
; Patent No. 5846538
;  GENERAL INFORMATION:
;    APPLICANT:  Cheever, Martin A.
;    APPLICANT:  Disis, Mary L.
;    TITLE OF INVENTION:  IMMUNE REACTIVITY TO HER-2/neu PROTEIN
;    TITLE OF INVENTION:  FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
;    TITLE OF INVENTION:  HER-2/neu ONCOGENE IS ASSOCIATED
;    NUMBER OF SEQUENCES:  69
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed and Berry LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  US
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/486,348A
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sharkey, Richard G.
;      REGISTRATION NUMBER:  32,629
;      REFERENCE/DOCKET NUMBER:  920010.448C6
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  29:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
US-08-486-348A-29

  Query Match             100.0%;  Score 51;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.0097;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db          1 VMAGVGSPYV 10


RESULT 4
US-08-468-545B-29
; Sequence 29, Application US/08468545B
; Patent No. 5876712
;  GENERAL INFORMATION:
;    APPLICANT:  Cheever, Martin A.
;    APPLICANT:  Disis, Mary L.
;    TITLE OF INVENTION:  IMMUNE REACTIVITY TO HER-2/neu PROTEIN
;    TITLE OF INVENTION:  FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
;    TITLE OF INVENTION:  HER-2/neu ONCOGENE IS ASSOCIATED
;    NUMBER OF SEQUENCES:  69
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed and Berry LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  US
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/468,545B
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sharkey, Richard G.
;      REGISTRATION NUMBER:  32,629
;      REFERENCE/DOCKET NUMBER:  920010.448C5
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  29:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
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;      TOPOLOGY: linear
US-08-468-545B-29

  Query Match             100.0%;  Score 51;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.0097;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db          1 VMAGVGSPYV 10


RESULT 5
US-08-466-680B-29
; Sequence 29, Application US/08466680B
; Patent No. 6075122
;  GENERAL INFORMATION:
;    APPLICANT:  Cheever, Martin A.
;    APPLICANT:  Disis, Mary L.
;    TITLE OF INVENTION:  IMMUNE REACTIVITY TO HER-2/neu PROTEIN
;    TITLE OF INVENTION:  FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
;    TITLE OF INVENTION:  HER-2/neu ONCOGENE IS ASSOCIATED
;    NUMBER OF SEQUENCES:  69
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed and Berry LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  US
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/466,680B
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sharkey, Richard G.
;      REGISTRATION NUMBER:  32,629
;      REFERENCE/DOCKET NUMBER:  920010.448C4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  29:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
US-08-466-680B-29

  Query Match             100.0%;  Score 51;  DB 2;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.0097;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db          1 VMAGVGSPYV 10


RESULT 6
US-09-341-982-95
; Sequence 95, Application US/09341982
; Patent No. 6558671
; GENERAL INFORMATION:
;  APPLICANT: SLINGLUFF, Craig L.
;  APPLICANT: HUNT, Donald F.
;  APPLICANT: ENGELHARD, Victor H.
;  APPLICANT: KITTLESEN, David
;  TITLE OF INVENTION: CYSTEINE-DEPLETED PEPTIDES RECOGNIZED BY A3-RESTRICTED
;  TITLE OF INVENTION: CYTOTOXIC LYMPHOCYTES, AND USES THEREFOR
;  FILE REFERENCE: SLINGLUFF=3B
;  CURRENT APPLICATION NUMBER: US/09/341,982
;  CURRENT FILING DATE: 1999-09-20
;  EARLIER APPLICATION NUMBER: PCT/US98/01592
;  EARLIER FILING DATE: 1998-01-29
;  EARLIER APPLICATION NUMBER: 60/037,781
;  EARLIER FILING DATE: 1997-01-31
;  NUMBER OF SEQ ID NOS: 104
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 95
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Fragment of
;   OTHER INFORMATION: human protein
US-09-341-982-95

  Query Match             100.0%;  Score 51;  DB 2;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.0097;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db          1 VMAGVGSPYV 10


RESULT 7
US-09-543-608A-16
; Sequence 16, Application US/09543608A
; Patent No. 6602510
; GENERAL INFORMATION:
;  APPLICANT: Fikes, John D.
;  APPLICANT:  Sette, Alessandro
;  APPLICANT:  Sidney, John
;  APPLICANT:  Southwood, Scott
;  APPLICANT:  Celis, Esteban
;  APPLICANT:  Keogh, Elissa A.
;  APPLICANT:  Chesnut, Robert
;  APPLICANT:  Epimmune Inc.
;  TITLE OF INVENTION: HLA Class I A2 Tumor Associated Antigen
;  TITLE OF INVENTION:  Peptides and Vaccine Compositions
;  FILE REFERENCE: 018623-015710US
;  CURRENT APPLICATION NUMBER: US/09/543,608A
;  CURRENT FILING DATE:  2002-04-05
;  NUMBER OF SEQ ID NOS: 52
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 16
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Her2/neu.773
US-09-543-608A-16

  Query Match             100.0%;  Score 51;  DB 2;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.0097;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db          1 VMAGVGSPYV 10


RESULT 8
US-09-354-533-29
; Sequence 29, Application US/09354533
; Patent No. 6664370
;   GENERAL INFORMATION:
;        APPLICANT: Cheever, Martin A.
;                   Disis, Mary L.
;        TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
```

; FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/354,533
; FILING DATE: 15-Jul-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C9
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-09-354-533-29

Query Match 100.0%; Score 51; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0097;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VMAGVGSPYV 10
||||||||||
Db 1 VMAGVGSPYV 10

RESULT 9
PCT-US95-16415-12
; Sequence 12, Application PC/TUS9516415
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: IN VIVO ACTIVATION OF TUMOR-SPECIFIC
; TITLE OF INVENTION: CYTOTOXIC T CELLS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute
; STREET: 10666 North Torrey Pines Road, TPC-8
; CITY: La Jolla
; STATE: California
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/16415
; FILING DATE: 13-DEC-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/355,558
; FILING DATE: 14-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Logan, April C.
; REGISTRATION NUMBER: 33,950
; REFERENCE/DOCKET NUMBER: 433.1PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 554-2937
; TELEFAX: (619) 554-6312
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US95-16415-12

Query Match 100.0%; Score 51; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0097;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VMAGVGSPYV 10
||||||||||
Db 1 VMAGVGSPYV 10

RESULT 10
US-09-527-487-9
; Sequence 9, Application US/09527487
; Patent No. 6528060
; GENERAL INFORMATION:
; APPLICANT: Nicolette, Charles
; TITLE OF INVENTION: HER2 ANTIGENIC PEPTIDES
; FILE REFERENCE: 126881309200
; CURRENT APPLICATION NUMBER: US/09/527,487
; CURRENT FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-527-487-9

Query Match 92.2%; Score 47; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 MAGVGSPYV 10
|||||||||
Db 1 MAGVGSPYV 9

RESULT 11
US-08-159-339A-263
; Sequence 263, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 263:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-159-339A-263

Query Match 92.2%; Score 47; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VMAGVGSPY 9
||||||||| |
Db 2 VMAGVGSPY 10

RESULT 12
US-08-725-736D-10
; Sequence 10, Application US/08725736D
; Patent No. 5831016
; GENERAL INFORMATION:
; APPLICANT: WANG, R.F.; ROSENBERG, S. A.
; TITLE OF INVENTION: IDENTIFICATION OF TRP-2 AS
; TITLE OF INVENTION: A HUMAN TUMOR ANTIGEN RECOGNIZED BY CYTOTOXIC T
; TITLE OF INVENTION: LYMPHOCYTES
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/725,736D
; FILING DATE: 04-OCT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/599,602
; FILING DATE: 09-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
; REGISTRATION NUMBER: 36,434
; REFERENCE/DOCKET NUMBER: 2026-4243
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9
; TYPE: AMINO ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: UNKNOWN
; MOLECULE TYPE:
; DESCRIPTION: PEPTIDE
; FEATURE:
; NAME/KEY: TRP-2 PEPTIDE VARIANT
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
US-08-725-736D-10

Query Match 56.9%; Score 29; DB 1; Length 9;
Best Local Similarity 62.5%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 MAGVGSPY 9
:|| | ||
Db 1 LAGPGRPY 8

RESULT 13
US-09-162-368B-10
; Sequence 10, Application US/09162368B
; Patent No. 6083703
; GENERAL INFORMATION:
; APPLICANT: WANG, R.F.; ROSENBERG, S. A.
; TITLE OF INVENTION: IDENTIFICATION OF TRP-2 AS
; TITLE OF INVENTION: A HUMAN TUMOR ANTIGEN RECOGNIZED BY CYTOTOXIC T
; TITLE OF INVENTION: LYMPHOCYTES
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MICROSOFT WORD 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/162,368B
; FILING DATE: 28-SEPT-1998
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/725,736
; FILING DATE: 04-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/599,602
; FILING DATE: 09-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: KATHRYN M. BROWN
; REGISTRATION NUMBER: 34,556
; REFERENCE/DOCKET NUMBER: 2026-4243US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9
; TYPE: AMINO ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: UNKNOWN
; MOLECULE TYPE:
; DESCRIPTION: PEPTIDE

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;    FEATURE:
;      NAME/KEY:  TRP-2 PEPTIDE VARIANT
;      LOCATION:
;      IDENTIFICATION METHOD:
;      OTHER INFORMATION:
US-09-162-368B-10

  Query Match             56.9%;  Score 29;  DB 2;  Length 9;
  Best Local Similarity   62.5%;  Pred. No. 4.6e+05;
  Matches    5;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 MAGVGSPY 9
              :|| | ||
Db          1 LAGPGRPY 8


RESULT 14
US-09-161-877B-10
; Sequence 10, Application US/09161877B
; Patent No. 6132980
;  GENERAL INFORMATION:
;    APPLICANT:  WANG, R.F.; ROSENBERG, S. A.
;    TITLE OF INVENTION:  IDENTIFICATION OF TRP-2
;    TITLE OF INVENTION:  AS A HUMAN TUMOR ANTIGEN RECOGNIZED BY
;    TITLE OF INVENTION:  CYTOTOXIC T LYMPHOCYTES
;    NUMBER OF SEQUENCES:  32
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORGAN & FINNEGAN, L.L.P.
;      STREET:  345 PARK AVENUE
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  10154
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  FLOPPY DISK
;      COMPUTER:  IBM PC COMPATIBLE
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  MICROSOFT WORD 97
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/161,877B
;      FILING DATE:  28-SEPT-1998
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/725,736
;      FILING DATE:  04-OCT-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/599,602
;      FILING DATE:  09-FEB-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KATHRYN M. BROWN
;      REGISTRATION NUMBER:  34,556
;      REFERENCE/DOCKET NUMBER:  2026-4243US2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 758-4800
;      TELEFAX:  (212) 751-6849
;      TELEX:  421792
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9
;      TYPE:  AMINO ACID
;      STRANDEDNESS:  SINGLE
;      TOPOLOGY:  UNKNOWN
;    MOLECULE TYPE:
;      DESCRIPTION:  PEPTIDE
;    FEATURE:
;      NAME/KEY:  TRP-2 PEPTIDE VARIANT
;      LOCATION:
;      IDENTIFICATION METHOD:
;      OTHER INFORMATION:
US-09-161-877B-10

  Query Match             56.9%;  Score 29;  DB 2;  Length 9;
  Best Local Similarity   62.5%;  Pred. No. 4.6e+05;
  Matches    5;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 MAGVGSPY 9
              :|| | ||
Db          1 LAGPGRPY 8


RESULT 15
US-08-172-707-5
; Sequence 5, Application US/08172707
; Patent No. 5455168
;  GENERAL INFORMATION:
;    APPLICANT:  MARUTA, Kazuhiko
;    APPLICANT:  KUBOTA, Michio
;    APPLICANT:  SUGIMOTO, Toshiyuki
;    APPLICANT:  MIYAKE, Toshio
;    TITLE OF INVENTION:  NON-REDUCING SACCHARIDE-FORMING ENZYME,
;    TITLE OF INVENTION:  AND ITS PREPARATION AND USES
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/172,707
;      FILING DATE:  12-DEC-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 362131/1992
;      FILING DATE:  28-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 265416/1993
;      FILING DATE:  30-SEP-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  TOWNSEND, G. Kevin
;      REGISTRATION NUMBER:  34,033
;      REFERENCE/DOCKET NUMBER:  MARUTA=1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;      TELEX:  248633
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-172-707-5

  Query Match             52.9%;  Score 27;  DB 1;  Length 10;
  Best Local Similarity   83.3%;  Pred. No. 1.5e+02;
  Matches    5;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 GVGSPY 9
              | ||||
Db          2 GRGSPY 7


Search completed: April 11, 2006, 19:24:09
Job time : 46 secs
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OM protein - protein search, using sw model

Run on: April 11, 2006, 19:23:29 ; Search time 163 Seconds
(without alignments)
25.634 Million cell updates/sec

Title: US-09-277-064-12
Perfect score: 51
Sequence: 1 VMAGVGSPYV 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 232507

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	51	100.0	10	2	US-08-812-393A-49	Sequence 49, Appl
2	51	100.0	10	3	US-09-354-533-29	Sequence 29, Appl
3	51	100.0	10	3	US-09-277-074-12	Sequence 12, Appl
4	51	100.0	10	3	US-09-277-064-12	Sequence 12, Appl
5	51	100.0	10	3	US-09-774-681-49	Sequence 49, Appl
6	51	100.0	10	4	US-10-080-013-16	Sequence 16, Appl
7	51	100.0	10	4	US-10-245-871-620	Sequence 620, App
8	51	100.0	10	4	US-10-149-138-786	Sequence 786, App
9	51	100.0	10	4	US-10-149-138-2352	Sequence 2352, Ap
10	51	100.0	10	4	US-10-149-138-4335	Sequence 4335, Ap
11	51	100.0	10	4	US-10-149-138-4422	Sequence 4422, Ap
12	51	100.0	10	4	US-10-149-138-4435	Sequence 4435, Ap
13	51	100.0	10	4	US-10-253-286-620	Sequence 620, App
14	51	100.0	10	4	US-10-289-566-16	Sequence 16, Appl
15	51	100.0	10	4	US-10-333-430-31	Sequence 31, Appl
16	51	100.0	10	4	US-10-647-005-29	Sequence 29, Appl
17	51	100.0	10	4	US-10-149-138-786	Sequence 786, App
18	51	100.0	10	4	US-10-149-138-2352	Sequence 2352, Ap
19	51	100.0	10	4	US-10-149-138-4335	Sequence 4335, Ap
20	51	100.0	10	4	US-10-149-138-4422	Sequence 4422, Ap
21	51	100.0	10	4	US-10-149-138-4435	Sequence 4435, Ap
22	51	100.0	10	6	US-11-121-347-29	Sequence 29, Appl
23	47	92.2	9	4	US-10-338-730-9	Sequence 9, Appli
24	47	92.2	9	4	US-10-149-138-60	Sequence 60, Appl
25	47	92.2	9	4	US-10-149-138-520	Sequence 520, App
26	47	92.2	9	4	US-10-149-138-1413	Sequence 1413, Ap
27	47	92.2	9	4	US-10-149-138-1891	Sequence 1891, Ap
28	47	92.2	9	4	US-10-149-138-2351	Sequence 2351, Ap
29	47	92.2	9	4	US-10-149-138-2441	Sequence 2441, Ap
30	47	92.2	9	4	US-10-149-138-3129	Sequence 3129, Ap
31	47	92.2	9	4	US-10-149-138-3616	Sequence 3616, Ap
32	47	92.2	9	4	US-10-149-138-3962	Sequence 3962, Ap
33	47	92.2	9	4	US-10-149-138-60	Sequence 60, Appl
34	47	92.2	9	4	US-10-149-138-520	Sequence 520, App
35	47	92.2	9	4	US-10-149-138-1413	Sequence 1413, Ap
36	47	92.2	9	4	US-10-149-138-1891	Sequence 1891, Ap
37	47	92.2	9	4	US-10-149-138-2351	Sequence 2351, Ap
38	47	92.2	9	4	US-10-149-138-2441	Sequence 2441, Ap
39	47	92.2	9	4	US-10-149-138-3129	Sequence 3129, Ap
40	47	92.2	9	4	US-10-149-138-3616	Sequence 3616, Ap
41	47	92.2	9	4	US-10-149-138-3962	Sequence 3962, Ap
42	47	92.2	10	4	US-10-149-138-97	Sequence 97, Appl
43	47	92.2	10	4	US-10-149-138-1455	Sequence 1455, Ap
44	47	92.2	10	4	US-10-149-138-2385	Sequence 2385, Ap
45	47	92.2	10	4	US-10-149-138-3174	Sequence 3174, Ap

ALIGNMENTS

RESULT 1
US-08-812-393A-49
; Sequence 49, Application US/08812393A
; Publication No. US20010007152A1
; GENERAL INFORMATION:
; APPLICANT: SHERMAN, Linda A.
; APPLICANT: LUSTGARTEN, Joseph
; TITLE OF INVENTION: RECOMBINANT CONSTRUCTS ENCODING
; TITLE OF INVENTION: T CELL RECEPTORS SPECIFIC FOR HUMAN HLA-RESTRICTED TUMOR
; TITLE OF INVENTION: ANTIGENS
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/812,393A
; FILING DATE: 05-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 31333-20001.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; TELEFAX: 202-822-0168
; TELEX:
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-812-393A-49

Query Match 100.0%; Score 51; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 VMAGVGSPYV 10
              ||||||||||
Db          1 VMAGVGSPYV 10


RESULT 2
US-09-354-533-29
; Sequence 29, Application US/09354533
; Publication No. US20020055614A1
;   GENERAL INFORMATION:
;        APPLICANT: Cheever, Martin A.
;                   Disis, Mary L.
;        TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
;                            FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
;                            HER-2/neu ONCOGENE IS ASSOCIATED
;        NUMBER OF SEQUENCES: 69
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Seed and Berry LLP
;             STREET: 6300 Columbia Center, 701 Fifth Avenue
;             CITY: Seattle
;             STATE: Washington
;             COUNTRY: US
;             ZIP: 98104-7092
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/354,533
;             FILING DATE: 15-Jul-1999
;             CLASSIFICATION: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Sharkey, Richard G.
;             REGISTRATION NUMBER: 32,629
;             REFERENCE/DOCKET NUMBER: 920010.448C9
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (206) 622-4900
;             TELEFAX: (206) 682-6031
;   INFORMATION FOR SEQ ID NO: 29:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 10 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-09-354-533-29

  Query Match             100.0%;  Score 51;  DB 3;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.016;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db          1 VMAGVGSPYV 10


RESULT 3
US-09-277-074-12
; Sequence 12, Application US/09277074
; Publication No. US20030022820A1
; GENERAL INFORMATION:
;  APPLICANT:  Sherman, Linda A.
;  TITLE OF INVENTION:  IN VIVO ACTIVATION OF TUMOR-SPECIFIC CYTOTOXIC T CELLS
;  FILE REFERENCE:  SCR2155S
;  CURRENT APPLICATION NUMBER: US/09/277,074
;  CURRENT FILING DATE:  1999-03-26
;  PRIOR APPLICATION NUMBER:  08/355,558
;  PRIOR FILING DATE:  1994-12-14
;  PRIOR APPLICATION NUMBER:  PCT/US95/16415
;  PRIOR FILING DATE:  1995-12-14
;  NUMBER OF SEQ ID NOS:  39
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 12
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-277-074-12

  Query Match             100.0%;  Score 51;  DB 3;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.016;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db          1 VMAGVGSPYV 10


RESULT 4
US-09-277-064-12
; Sequence 12, Application US/09277064
; Publication No. US20030064916A1
; GENERAL INFORMATION:
;  APPLICANT:  Sherman, Linda A.
;  TITLE OF INVENTION:  IN VIVO ACTIVATION OF TUMOR-SPECIFIC CYTOTOXIC T CELLS
;  FILE REFERENCE:  SCR2152S
;  CURRENT APPLICATION NUMBER: US/09/277,064
;  CURRENT FILING DATE:  1999-03-26
;  PRIOR APPLICATION NUMBER:  08/355,558
;  PRIOR FILING DATE:  1994-12-14
;  PRIOR APPLICATION NUMBER:  PCT/US95/16415
;  PRIOR FILING DATE:  1995-12-14
;  NUMBER OF SEQ ID NOS:  39
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 12
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-277-064-12

  Query Match             100.0%;  Score 51;  DB 3;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.016;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db          1 VMAGVGSPYV 10


RESULT 5
US-09-774-681-49
; Sequence 49, Application US/09774681
; Publication No. US20030208780A1
; GENERAL INFORMATION:
;  APPLICANT: Sunol Molecular Corporatiopn
;  APPLICANT:  Sherman, Linda
;  APPLICANT:  Lustgarten, Joseph
;  TITLE OF INVENTION: RECOMBINANT CONSTRUCTS ENCODING T CELL
;  TITLE OF INVENTION:  RECEPTORS SPECIFIC FOR HUMAN HLA-RESTRICTED TUMOR ANTIGENS
;  FILE REFERENCE: 31333-20001.01
;  CURRENT APPLICATION NUMBER: US/09/774,681
;  CURRENT FILING DATE:  2001-02-01
;  PRIOR APPLICATION NUMBER: US 08/812,393
;  PRIOR FILING DATE: 1997-03-05
;  PRIOR APPLICATION NUMBER: US 60/012,845
;  PRIOR FILING DATE: 1996-03-05
;  NUMBER OF SEQ ID NOS: 65
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 49
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthesized peptide
US-09-774-681-49
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  Query Match           100.0%;  Score 51;  DB 3;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0.016;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db          1 VMAGVGSPYV 10


RESULT 6
US-10-080-013-16
; Sequence 16, Application US/10080013
; Publication No. US20030077248A1
; GENERAL INFORMATION:
;  APPLICANT: Moriarty, Ann
;  APPLICANT:  Leturcq, Didier
;  APPLICANT:  Degraw, Juli
;  APPLICANT:  Heiskala, Marja
;  APPLICANT:  Peterson, Per
;  APPLICANT:  Jackson, Michael
;  TITLE OF INVENTION: A CELL THERAPY METHOD FOR THE TREATMENT OF TUMORS
;  FILE REFERENCE: ORT-1557
;  CURRENT APPLICATION NUMBER: US/10/080,013
;  CURRENT FILING DATE:  2002-02-19
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-080-013-16

  Query Match           100.0%;  Score 51;  DB 4;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0.016;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db          1 VMAGVGSPYV 10


RESULT 7
US-10-245-871-620
; Sequence 620, Application US/10245871
; Publication No. US20030235594A1
; GENERAL INFORMATION:
;  APPLICANT: HUMPHREYS, ROBERT
;  APPLICANT:  XU, MINZHEN
;  TITLE OF INVENTION: Ii-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
;  FILE REFERENCE: REH-2013
;  CURRENT APPLICATION NUMBER: US/10/245,871
;  CURRENT FILING DATE:  2003-01-09
;  PRIOR APPLICATION NUMBER: 10/197,000
;  PRIOR FILING DATE: 2002-07-17
;  PRIOR APPLICATION NUMBER: 09/396,813
;  PRIOR FILING DATE: 1999-09-14
;  NUMBER OF SEQ ID NOS: 905
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 620
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-245-871-620

  Query Match           100.0%;  Score 51;  DB 4;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0.016;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db          1 VMAGVGSPYV 10


RESULT 8
US-10-149-138-786
; Sequence 786, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
;  APPLICANT: Fikes, John
;  APPLICANT:  Sette, Alessandro
;  APPLICANT:  Sidney, John
;  APPLICANT:  Southwood, Scott
;  APPLICANT:  Chesnut, Robert
;  APPLICANT:  Celis, Esteban
;  APPLICANT:  Keogh, Elissa
;  TITLE OF INVENTION: Inducing Cellular Immune Responses to
;  TITLE OF INVENTION:  HER2/neu Using Peptide and Nucleic Acid Compositions
;  FILE REFERENCE: 2060.0140001
;  CURRENT APPLICATION NUMBER: US/10/149,138
;  CURRENT FILING DATE:  2002-06-10
;  PRIOR APPLICATION NUMBER: PCT/US00/33591
;  PRIOR FILING DATE: 2000-12-11
;  PRIOR APPLICATION NUMBER: US 09/458,299
;  PRIOR FILING DATE: 1999-12-11
;  NUMBER OF SEQ ID NOS: 4641
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 786
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-786

  Query Match           100.0%;  Score 51;  DB 4;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0.016;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db          1 VMAGVGSPYV 10


RESULT 9
US-10-149-138-2352
; Sequence 2352, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
;  APPLICANT: Fikes, John
;  APPLICANT:  Sette, Alessandro
;  APPLICANT:  Sidney, John
;  APPLICANT:  Southwood, Scott
;  APPLICANT:  Chesnut, Robert
;  APPLICANT:  Celis, Esteban
;  APPLICANT:  Keogh, Elissa
;  TITLE OF INVENTION: Inducing Cellular Immune Responses to
;  TITLE OF INVENTION:  HER2/neu Using Peptide and Nucleic Acid Compositions
;  FILE REFERENCE: 2060.0140001
;  CURRENT APPLICATION NUMBER: US/10/149,138
;  CURRENT FILING DATE:  2002-06-10
;  PRIOR APPLICATION NUMBER: PCT/US00/33591
;  PRIOR FILING DATE: 2000-12-11
;  PRIOR APPLICATION NUMBER: US 09/458,299
;  PRIOR FILING DATE: 1999-12-11
;  NUMBER OF SEQ ID NOS: 4641
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2352
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-2352

  Query Match           100.0%;  Score 51;  DB 4;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0.016;
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  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db          1 VMAGVGSPYV 10


RESULT 10
US-10-149-138-4335
; Sequence 4335, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
;  APPLICANT: Fikes, John
;  APPLICANT:  Sette, Alessandro
;  APPLICANT:  Sidney, John
;  APPLICANT:  Southwood, Scott
;  APPLICANT:  Chésnut, Robert
;  APPLICANT:  Celis, Esteban
;  APPLICANT:  Keogh, Elissa
;  TITLE OF INVENTION: Inducing Cellular Immune Responses to
;  TITLE OF INVENTION:  HER2/neu Using Peptide and Nucleic Acid Compositions
;  FILE REFERENCE: 2060.0140001
;  CURRENT APPLICATION NUMBER: US/10/149,138
;  CURRENT FILING DATE:  2002-06-10
;  PRIOR APPLICATION NUMBER: PCT/US00/33591
;  PRIOR FILING DATE: 2000-12-11
;  PRIOR APPLICATION NUMBER: US 09/458,299
;  PRIOR FILING DATE: 1999-12-11
;  NUMBER OF SEQ ID NOS: 4641
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4335
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Artificial Peptide
US-10-149-138-4335

  Query Match             100.0%;  Score 51;  DB 4;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.016;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db          1 VMAGVGSPYV 10


RESULT 11
US-10-149-138-4422
; Sequence 4422, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
;  APPLICANT: Fikes, John
;  APPLICANT:  Sette, Alessandro
;  APPLICANT:  Sidney, John
;  APPLICANT:  Southwood, Scott
;  APPLICANT:  Chesnut, Robert
;  APPLICANT:  Celis, Esteban
;  APPLICANT:  Keogh, Elissa
;  TITLE OF INVENTION: Inducing Cellular Immune Responses to
;  TITLE OF INVENTION:  HER2/neu Using Peptide and Nucleic Acid Compositions
;  FILE REFERENCE: 2060.0140001
;  CURRENT APPLICATION NUMBER: US/10/149,138
;  CURRENT FILING DATE:  2002-06-10
;  PRIOR APPLICATION NUMBER: PCT/US00/33591
;  PRIOR FILING DATE: 2000-12-11
;  PRIOR APPLICATION NUMBER: US 09/458,299
;  PRIOR FILING DATE: 1999-12-11
;  NUMBER OF SEQ ID NOS: 4641
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4422
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Artificial Peptide
US-10-149-138-4422

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  Best Local Similarity   100.0%;  Pred. No. 0.016;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db          1 VMAGVGSPYV 10


RESULT 12
US-10-149-138-4435
; Sequence 4435, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
;  APPLICANT: Fikes, John
;  APPLICANT:  Sette, Alessandro
;  APPLICANT:  Sidney, John
;  APPLICANT:  Southwood, Scott
;  APPLICANT:  Chesnut, Robert
;  APPLICANT:  Celis, Esteban
;  APPLICANT:  Keogh, Elissa
;  TITLE OF INVENTION: Inducing Cellular Immune Responses to
;  TITLE OF INVENTION:  HER2/neu Using Peptide and Nucleic Acid Compositions
;  FILE REFERENCE: 2060.0140001
;  CURRENT APPLICATION NUMBER: US/10/149,138
;  CURRENT FILING DATE:  2002-06-10
;  PRIOR APPLICATION NUMBER: PCT/US00/33591
;  PRIOR FILING DATE: 2000-12-11
;  PRIOR APPLICATION NUMBER: US 09/458,299
;  PRIOR FILING DATE: 1999-12-11
;  NUMBER OF SEQ ID NOS: 4641
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4435
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Artificial Peptide
US-10-149-138-4435

  Query Match             100.0%;  Score 51;  DB 4;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.016;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db          1 VMAGVGSPYV 10


RESULT 13
US-10-253-286-620
; Sequence 620, Application US/10253286
; Publication No. US20040058881A1
; GENERAL INFORMATION:
;  APPLICANT: HUMPHREYS, ROBERT
;  APPLICANT:  XU, MINZHEN
;  TITLE OF INVENTION: Ii-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
;  FILE REFERENCE: REH-2015
;  CURRENT APPLICATION NUMBER: US/10/253,286
;  CURRENT FILING DATE:  2003-01-13
;  PRIOR APPLICATION NUMBER: 10/197,000
;  PRIOR FILING DATE: 2002-07-17
;  PRIOR APPLICATION NUMBER: 09/396,813
;  PRIOR FILING DATE: 1999-09-14
;  NUMBER OF SEQ ID NOS: 905
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 620
;   LENGTH: 10
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;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-253-286-620

  Query Match             100.0%;  Score 51;  DB 4;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.016;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db          1 VMAGVGSPYV 10


RESULT 14
US-10-289-566-16
; Sequence 16, Application US/10289566
; Publication No. US20040071671A1
; GENERAL INFORMATION:
;  APPLICANT: Leturcq, Didier J.
;  APPLICANT:  Moriarty, Ann M.
;  APPLICANT:  Jackson, Michael R.
;  APPLICANT:  Peterson, Per A.
;  APPLICANT:  Richards, Jon M.
;  TITLE OF INVENTION: A CELL THERAPY METHOD FOR THE TREATMENT OF TUMORS
;  FILE REFERENCE: ORT 1342CIP
;  CURRENT APPLICATION NUMBER: US/10/289,566
;  CURRENT FILING DATE:  2002-11-07
;  PRIOR APPLICATION NUMBER: US 60/270,252
;  PRIOR FILING DATE: 2001-02-20
;  PRIOR APPLICATION NUMBER: US 10/080,013
;  PRIOR FILING DATE: 2002-02-19
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-289-566-16

  Query Match             100.0%;  Score 51;  DB 4;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.016;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
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Db          1 VMAGVGSPYV 10


RESULT 15
US-10-333-430-31
; Sequence 31, Application US/10333430
; Publication No. US20040072240A1
; GENERAL INFORMATION:
;  APPLICANT: INSERM
;  APPLICANT:  INSTITUT GUSTAVE ROUSSY
;  APPLICANT:  KOSMATOPOULOS, Kostas
;  APPLICANT:  TOURDOT, Sophie
;  APPLICANT:  SCARDINO, Antonio
;  APPLICANT:  GROSS, David, Alexandre
;  TITLE OF INVENTION: METHOD FOR SCREENING PEPTIDES FOR USE IN
;  TITLE OF INVENTION:  IMMUNOTHERAPY
;  FILE REFERENCE: 33339/259034
;  CURRENT APPLICATION NUMBER: US/10/333,430
;  CURRENT FILING DATE:  2003-10-02
;  PRIOR APPLICATION NUMBER: FR 0009591
;  PRIOR FILING DATE: 2000-07-21
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic peptide
US-10-333-430-31

  Query Match             100.0%;  Score 51;  DB 4;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.016;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VMAGVGSPYV 10
              ||||||||||
Db          1 VMAGVGSPYV 10


Search completed: April 11, 2006, 19:26:58
Job time : 164 secs
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